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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:05:26 ; Search time 81.32 Seconds
(without alignments)
8.198 Million cell updates/sec

Title: US-09-720-469-2
Perfect score: 50
Sequence: 1 DFMIGGDF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	9	21	AA19922
2	50	100.0	9	22	AA19931
3	50	100.0	166	21	AAG00090
4	50	100.0	183	21	AA196701
5	50	100.0	211	22	AA193302
6	50	100.0	212	14	AA193302
7	50	100.0	212	14	AA192048
8	50	100.0	216	22	AA193301
9	50	100.0	252	21	AAG16463
10	50	100.0	254	21	AAG05073
11	50	100.0	254	21	AAG16462

12	50	100.0	259	21	AAG05072	Arabidopsis thalia
13	50	100.0	260	21	AAG16461	Arabidopsis thalia
14	50	100.0	291	12	AA193878	Human cancer assoc
15	48	96.0	162	12	AA190764	Yeast peptidyl-pro
16	48	96.0	162	16	AA192962	Yeast peptidyl-pro
17	48	96.0	162	16	AA192918	Yeast peptidyl-pro
18	47	94.0	9	21	AA196963	Human cyclophilin
19	47	94.0	9	22	AA196963	Human cyclophilin
20	45	90.0	180	19	AA190784	D. discoideum cycl
21	45	90.0	269	22	AA194140	Human nuclear-spec
22	45	90.0	589	16	AA194292	B. malayi cyclophil
23	45	90.0	982	12	AA193320	Marine Natural Kil
24	45	90.0	1023	12	AA193319	Human cyclophilin
25	44	88.0	9	21	AA196958	Human cyclophilin
26	44	88.0	113	21	AAG03983	Human secreted pro
27	44	88.0	125	21	AAG18027	Arabidopsis thalia
28	44	88.0	129	21	AAG54741	Arabidopsis thalia
29	44	88.0	166	22	AA191215	Arabidopsis thalia
30	44	88.0	178	22	AA1975471	Human colon cancer
31	44	88.0	191	21	AA195070	Human PRO4984 poly
32	44	88.0	192	21	AAG48166	Arabidopsis thalia
33	44	88.0	201	21	AAG29380	Arabidopsis thalia
34	44	88.0	205	21	AAG15069	Arabidopsis thalia
35	44	88.0	206	21	AA1948165	Arabidopsis thalia
36	44	88.0	218	21	AAG29379	Arabidopsis thalia
37	44	88.0	228	21	AAG18026	Arabidopsis thalia
38	44	88.0	236	21	AAG18025	Arabidopsis thalia
39	44	88.0	370	20	AA194196	Arabidopsis thalia
40	43	86.0	171	22	AA194141	Mouse cyclophilin
41	43	86.0	987	22	AA194633	Caenorhabditis ele
42	42	84.0	152	21	AAG08983	Amino acid sequenc
43	42	84.0	204	21	AAG08982	Arabidopsis thalia
44	42	84.0	218	21	AAG08981	Arabidopsis thalia
45	41	82.0	21	16	AA1972925	Yeast pPase trypt

ALIGNMENTS

RESULT 1

AA196922

ID AA196922 standard; peptide; 9 AA.

XX

AC AA196922;

XX

DT 11-APR-2000 (first entry)

XX

DE Human cyclophilin B peptide fragment #2.

XX

DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

KW HLA antigen; diagnosis; tumour; therapy.

XX

OS Homo sapiens.

XX

XX WO9967288-A1.

PN

PD 29-DEC-1999.

XX

PF 24-JUN-1999; 99WO-JP03360.

XX

PR 25-JUN-1998; 98JP-0178449.

XX

XX (SUMU) SUMITOMO PHARM CO LTD.

PA (ITOH/) ITOH K.

XX

PI Itoh K, Gomi S;

XX

DR WPI; 2000-116932/10.

XX

XX Tumour antigen peptides derived from cyclophilin B for treatment and

PT diagnosis of tumours

XX

PS Claim 4; Page 49; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
| | | | | | | |
Db 1 dfmiqggdf 9

RESULT 2
AAB46931
ID AAB46931 standard; peptide; 9 AA.
XX AC AAB46931;
XX
XX 04-MAY-2001 (first entry)
XX
DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 17.
XX
XX Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW viricide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.
XX
XX Homo sapiens.
XX
XX EP1074267-A1.
XX
XX 07-FEB-2001.
XX
XX 24-JUL-2000; 2000EP-0306263.
XX
XX 22-JUL-1999; 99JP-0207687.
XX
XX (SUNU) SUMITOMO PHARM CO LTD.
XX
XX Takasu H, Gotoh M, Yamaoka T;
XX
XX WPI; 2001-193144/20.
XX
XX Use of antigenic proteins, peptides, interferon or their encoding DNA,
PT in the manufacture of an agent for the induction of antigen-specific T
PT cells -
XX
XX Disclosure: Page 15; 25pp; English.
XX
XX This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of
CC an agent for induction of antigen-specific T cells. The products of
CC the invention have virucide and cytostatic activity and can be used for
CC gene therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease.
XX
XX Sequence 9 AA;

Query Match 100.0%; Score 50; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
| | | | | | | |
Db 1 dfmiqggdf 9

RESULT 3
AAG00090
ID AAG00090 standard; Protein; 166 AA.
XX AC AAG00090;
XX
XX 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 4171.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX
XX (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX N-PSDB; AAC00096.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.
XX
XX Sequence 166 AA;

Query Match 100.0%; Score 50; DB 21; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
| | | | | | | |
Db 99 dfmiqggdf 107

RESULT 4
AAB56701

ID XX AAB56701 standard; Protein; 183 AA.
 AC XX AAB56701;
 DT XX
 DT XX 13-MAR-2001 (first entry)
 XX XX Human prostate cancer antigen protein sequence SEQ ID NO:1279.
 DE XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW XX neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW XX vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
 KW XX antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW XX gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW XX wound; infectious disease.
 XX XX Homo sapiens.
 OS XX
 XX XX WO200055174-A1.
 PN XX
 XX XX 21-SEP-2000.
 PD XX
 XX XX 08-MAR-2000; 2000WO-US05988.
 PF XX
 XX XX 12-MAR-1999; 99US-0124270.
 XX XX (HUMA-) HUMAN GENOME SCI INC.
 PA XX (ROSE/) ROSEN C A.
 XX XX Rosen CA, Ruben SM;
 PI XX
 XX XX WPI; 2000-587513/55.
 DR XX N-PSDB; AAF15904.
 DR XX
 XX XX Prostate cancer associated gene sequences, referred to as prostate
 PT XX cancer antigens, useful for treatment, prevention, and diagnosis of
 PT XX disorders such as prostate cancer -
 XX XX
 PS Claim 11; Page 1699-1700; 2338pp; English.
 XX XX
 CC AAF15566 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention.
 XX XX
 SQ Sequence 183 AA;

Query Match 100.0%; Score 50; DB 21; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM1QGGDF 9
 |||||
 Db 77 dfmiqggdf 85

RESULT 5
 AAB73302
 ID AAB73302 standard; protein; 211 AA.
 XX
 AC AAB73302;
 XX
 DT 22-MAY-2001 (first entry)

XX
 DE XX Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
 XX XX
 KW Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
 KW somatolactogenic function modulator; immunosuppression; short stature;
 KW muscle wasting; osteoporosis; HIV infection; breast cancer;
 KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia;
 KW C-terminal deletion mutant; mutein.
 XX XX
 OS Homo sapiens.
 XX XX
 PN WO200113113-A1.
 XX XX
 PD 22-FEB-2001.
 XX XX
 PF 10-AUG-2000; 2000WO-US21789.
 XX XX
 PR 19-AUG-1999; 99US-0149752.
 XX XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX XX
 PI Clevenger CV, Ryczyn MA;
 XX XX WPI; 2001-211249/21.
 DR XX
 XX XX Novel composition for modulating somatolactogenic function, comprises
 PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
 PT B with somatolactogenic hormone -
 PT XX
 PS Disclosure; Page 2; 21pp; English.
 XX XX
 CC The invention relates to a composition for modulating somatolactogenic
 CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B
 CC (particularly a CypB mutant in which residues 2-12 of the mature protein
 CC are absent) or an inhibitor of the interaction of cyclophilin B with a
 CC somatolactogenic hormone (e.g., prolactin, growth hormone). The invention
 CC also relates to a method of identifying inhibitors of somatolactogenic
 CC functions using CypB and a somatolactogenic hormone, and a method for
 CC diagnosing diseases associated with abnormal somatolactogenic functions
 CC by assessing CypB levels in a sample from a patient. Cyclophilin B is
 CC useful for augmenting somatolactogenic function in the animal, and
 CC cyclophilin B mutant or a composition comprising an inhibitor of the
 CC interaction of cyclophilin B with a somatolactogenic hormone, is useful
 CC for inhibiting somatolactogenic function in the animal. A composition
 CC comprising cyclophilin B is useful in the treatment of immunosuppression,
 CC in the treatment of short stature, muscle wasting and osteoporosis. A
 CC composition comprising cyclophilin B mutant or a composition comprising
 CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic
 CC hormone, is useful for treating HIV infection, breast and prostate
 CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
 CC sequence represents a human cyclophilin B C-terminal mutant, CypB-AIAKE.
 CC Note: The present sequence is not shown in the specification, but
 CC is derived from the wild-type CypB sequence shown on pages 17-18.
 XX XX
 SQ Sequence 211 AA;

Query Match 100.0%; Score 50; DB 22; Length 211;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM1QGGDF 9
 |||||
 Db 99 dfmiqggdf 107

RESULT 6
 AAR32353
 ID AAR32353 standard; Protein; 212 AA.
 XX
 AC AAR32353;
 XX
 DT 16-JUN-1993 (first entry)

```

XX DE Cyclophilin C.
XX KW Cyclophilin C; bone marrow; stromal cell line; AC 6; interleukin-1;
XX KW IL-1; cyp A; cyp B; peptidyl-prolyl isomerase; PPIase;
XX KW cyclosporin A; CsA; ligand; calcineurin.
XX OS Mus musculus.
XX PN W09303050-A.
XX PD 18-FEB-1993.
XX PF 05-AUG-1992; 92WO-US06462.
XX PR 05-AUG-1991; 91US-0740375.
XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX PI Friedman JS, Weissman IL;
XX DR WPI: 1993-076431/09.
XX DR N-PSDB; AAQ36841.
XX PT Cyclophilin C polypeptide and nucleic acid encoding it - useful
XX PT for screening a tissue-specific immunosuppressive agent
XX PS Claim 9; Page 46 + Fig 1; 63pp; English.
XX CC A third mammalian cyclophilin, cyp C, was isolated from a cDNA
XX CC library prepd. from the murine bone marrow derived stromal cell line
XX CC AC 6. This cDNA was isolated from a substracted sub-library contg.
XX CC genes induced by treatment of the stromal cell line with interleukin-
XX CC 1 (IL-1). The message levels for cyp C show a 2-3 fold induction by
XX CC treatment with IL-1, and this cDNA exhibits a high level of homology
XX CC with known cyclophilins. Cyp C is distinct from mammalian
XX CC cyclophilins A and B in both sequence and tissue distribution of
XX CC expression. A fusion protein contg., e.g. amino acids 16-212 of cyp C
XX CC possesses peptidyl-prolyl isomerase (PPIase) activity which can be
XX CC completely inhibited by addition of cyclosporin A (CsA). These cyp C
XX CC fusion proteins can be used as ligands for the identification of
XX CC intracellular proteins which together form high affinity associations.
XX CC For example, the cyp C fusion protein binds to a protein of 77 kD in
XX CC the absence of CsA, while in the presence fo CsA it no longer binds
XX CC to this p77, but instead binds specifically to a protein of 55 kD,
XX CC identified as calcineurin (U.S.S.N.07/740175).
XX SQ Sequence 212 AA;

Query Match 100.0%; Score 50; DB 14; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIOGGDF 9
Db 93 dfmiqggdf 101
|||||

RESULT 7
AA92048
ID AA92048 standard; Protein; 212 AA.
XX AC AA92048;
XX DT 01-AUG-2000 (first entry)
XX DE A. niger peptidyl-prolyl cis-trans isomerase (CYPB).
XX KW Cyclophilin-like peptidyl prolyl cis-trans isomerase; CYPB;
XX KW food processing; Endoplasmic retention signal; cis-trans isomerization;
XX KW protein secretion; toxin; ADP-glucose pyrophosphorylase; glucanase;
XX KW beta-1,4-endoglucanase.

XX OS Aspergillus niger.
XX FH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT Protein /label= signal_peptide
XX FT /label= mature_protein
XX PN W0200018934-A1.
XX PD 06-APR-2000.
XX PF 30-SEP-1999; 99WO-IB01669.
XX PR 30-SEP-1998; 98GB-0021198.
XX PA (DANI-) DANISCO AS.
XX PI Derkx PMF, Madrid SM;
XX DR WPI: 2000-293167/25.
XX DR N-PSDB; AAA08772.
XX PT New peptidyl prolyl cis-trans isomerase, designated CYPB, from
XX PT Aspergillus niger, useful in methods for increasing the yield of
XX PT secreted polypeptides, such as enzymes used in food processing, from
XX PT cells
XX PS Claim 13; Page 47-48; 52pp; English.
XX CC This sequence shows Aspergillus niger cyclophilin-like peptidyl prolyl
XX CC cis-trans isomerase (CYPB). CYPB is capable of catalyzing the cis-trans
XX CC isomerization of a peptide bond on the N-terminal side of proline
XX CC residues in polypeptides. CYPB are useful in methods for increasing the
XX CC yield of secreted polypeptides from cells. The secreted polypeptides may
XX CC be enzymes (such as chymosin, thaumatin or alpha-galactosidase) that can
XX CC be used in food processing, a pest toxin, adenosine diphosphate
XX CC (ADP)-glucose pyrophosphorylase, a glucanase or beta-1,4-endoglucanase.
XX SQ Sequence 212 AA;

Query Match 100.0%; Score 50; DB 21; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIOGGDF 9
Db 90 dfmiqggdf 98
|||||

RESULT 8
AAB73301
ID AAB73301 standard; protein; 216 AA.
XX AC AAB73301;
XX DT 22-MAY-2001 (first entry)
XX DE Human cyclophilin B (CypB).
XX KW Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
XX KW somatolactogenic function modulator; immunosuppression; short stature;
XX KW muscle wasting; osteoporosis; HIV infection; breast cancer;
XX KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
XX OS Homo sapiens.
XX PN W0200113113-A1.
XX PD 22-FEB-2001.

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PF 10-AUG-2000; 2000WO-US21789.
 XX PR 19-AUG-1999; 99US-0149752.
 XX PR (UYPE-) UNIV PENNSYLVANIA.
 XX PR 01-APR-1999; 99US-0127462.
 XX PR 06-APR-1999; 99US-0128234.
 XX PR 08-APR-1999; 99US-0128714.
 XX PR 16-APR-1999; 99US-0128845.
 XX PR 19-APR-1999; 99US-0130077.
 XX PR 21-APR-1999; 99US-0130449.
 XX PR 23-APR-1999; 99US-0130510.
 XX PR 28-APR-1999; 99US-0130891.
 XX PR 30-APR-1999; 99US-0131449.
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 XX PR 06-MAY-1999; 99US-0132486.
 XX PR 07-MAY-1999; 99US-0132487.
 XX PR 07-MAY-1999; 99US-0132863.
 XX PR 11-MAY-1999; 99US-0134256.
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 XX PR 14-MAY-1999; 99US-0134370.
 XX PR 18-MAY-1999; 99US-0134768.
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 XX PR 27-MAY-1999; 99US-0136392.
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 XX PR 01-JUL-1999; 99US-0141842.
 XX PR 01-JUL-1999; 99US-0142154.
 XX PR 02-JUL-1999; 99US-0142055.
 XX PR 06-JUL-1999; 99US-0142390.
 XX PR 08-JUL-1999; 99US-0142803.
 XX PR 09-JUL-1999; 99US-0142920.
 XX PR 12-JUL-1999; 99US-0142977.
 XX PR 13-JUL-1999; 99US-0143542.
 XX PR 14-JUL-1999; 99US-0143624.

PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0128845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 28-APR-1999; 99US-0130891.
 PR 30-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 30-APR-1999; 99US-0132407.
 PR 04-MAY-1999; 99US-0132484.
 PR 05-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 07-MAY-1999; 99US-0132487.
 PR 07-MAY-1999; 99US-0132863.
 PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
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 PR 20-MAY-1999; 99US-0135124.
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 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
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 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
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 PR 18-JUN-1999; 99US-0139458.
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 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
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 PR 21-JUN-1999; 99US-0139817.
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 PR 24-JUN-1999; 99US-0140695.
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 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.

The invention relates to a composition for modulating somatolactogenic function, comprising cyclophilin B (CypB), a mutant of cyclophilin B (particularly a CypB mutant in which residues 2-12 of the mature protein are absent) or an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone (e.g., prolactin, growth hormone). The invention also relates to a method of identifying inhibitors of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is useful for augmenting somatolactogenic function in the animal, and cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for inhibiting somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for treating HIV infection, breast and prostate cancer, gigantism/acromegaly, and hyperprolactinaemia. The present sequence represents human cyclophilin B.

Query Match 100.0%; Score 50; DB 22; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
 Db 99 dfmiqggdf 107

RESULT 9
 AAG16463
 ID AAG16463 standard; Protein; 252 AA.
 AC AAG16463;
 DT 17-OCT-2000 (first entry)
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 17119.
 DE Arabidopsis thaliana.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX EP1033405-A2.
 PN 06-SEP-2000.
 PD 25-FEB-2000; 2000EP-0301439.
 XX 25-FEB-1999; 99US-0121825.
 XX 05-MAR-1999; 99US-0123180.

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PR 15-JUL-1999; 99US-0144005.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
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PR 04-AUG-1999; 99US-0147204.
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PR 09-AUG-1999; 99US-0147935.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
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PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
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PR 21-OCT-1999; 99US-0160814.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 23-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 50; DB 21; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIQGGDF 9
Db 142 dfmiqggdf 150
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RESULT 10
AAG05073
ID AAG05073 standard; Protein; 254 AA.
XX
AC AAG05073;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1339.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 21-OCT-1999; 99US-0160814.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
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PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 50; DB 21; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
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Db 143 dfmiggdf 151

RESULT 11
AAG16462
ID AAG16462 standard; Protein: 254 AA.
XX AC AAG16462;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 17118.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
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XX PR 08-APR-1999; 99US-0128714.
XX PR 16-APR-1999; 99US-0129845.
XX PR 19-APR-1999; 99US-0130077.
XX PR 21-APR-1999; 99US-0130449.
XX PR 23-APR-1999; 99US-0130510.
XX PR 28-APR-1999; 99US-0130891.
XX PR 30-APR-1999; 99US-0131449.
XX PR 30-APR-1999; 99US-0132048.

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PR 01-JUL-1999; 99US-0141842.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
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PR 01-SEP-1999; 99US-0151930.
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PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162143.
PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 50; DB 21; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEMIQGGDF 9
Db 144 dfmiqggdf 152

RESULT 12
AAG05072
ID AAG05072 standard; Protein: 259 AA.
XX
AC AAG05072;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1338.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
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[illegible]

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PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 30-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154778.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
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PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 25-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 50; DB 21; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy 1 DFMIOGGDF 9
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Db 150 dfmiqgguf 158

RESULT 14
AAB43878
ID AAB43878 standard; Protein; 291 AA.
XX
AC AAB43878;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated protein sequence SEQ ID NO:1323.
XX
KW Human; cancer associated gene; cancer antigen; detection; cancer;
diagnosis; cytostatic; proliferative; vulnary; immunomodulator;
antidiabetic; antitachytic; antirheumatic; antiallergic; antiviral;
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
dermatological; neuroprotective; thrombolytic; coagulant; nontropic;
vasotropic; antipsoriatic; antidiabetic; antiallergic; antitachytic;
immune disorder; haematopoietic cell disorder; gene therapy; inflammation;
allergic reaction; graft versus host disease; autoimmune disorder;
haemostatic; thrombolytic; cardiovascular disorder; infection;
neurological disease; drug screening.
XX
OS Homo sapiens.
XX
PN WO2000055350-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05882.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
WPI; 2000-587533/55.
DR N-PSDB; AAC78087.
XX
PT Novel isolated nucleic acids comprising sequences encoding peptides
useful for treating or diagnosing e.g. cancer -
XX
PS Claim 11; Page 1974-1975; 2352pp; English.
XX
CC AAC77607 to AAC78448 encode the human cancer associated proteins given
in AAB43398 to AAB44239. The proteins can have activities based on the
tissues and cells the genes are expressed in. Example of activities
include: cytostatic; proliferative; vulnary; immunomodulator;
antidiabetic; antitachytic; antirheumatic; antiallergic; antiviral;
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
dermatological; neuroprotective; thrombolytic; coagulant; nontropic;
vasotropic; antipsoriatic; antidiabetic; antiallergic; antitachytic;
immune disorder; haematopoietic cell disorder; gene therapy; inflammation;
allergic reaction; graft versus host disease; autoimmune disorder;
haemostatic; thrombolytic; cardiovascular disorder; infection;
neurological disease; drug screening.
XX
CC ameliorating medical conditions and diagnosing pathological conditions.
XX
CC polynucleotides, polypeptides, antibodies, agonists and antagonists from
the present invention may be used to treat immune disorders by activating
or inhibiting the proliferation, differentiation or mobilisation of
immune cells, to treat disorders of haematopoietic cells, autoimmune
disorders, allergic reactions, graft versus host disease and organ
rejection, modulate haemostatic or thrombolytic activity, modulate
```


Tue Jan 15 13:46:29 2002

us-09-720-469-2.rag

Db 57 dfmlqggdf 65

CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB4240 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 291 AA;

Query Match 100.0%; Score 50; DB 21; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.33; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

OY 1 DFMIQGGDF 9
| | | | | | | | |
Db 174 dfmlqggdf 182

RESULT 15
AAR10764
ID AAR10764 standard; Protein: 162 AA.
XX
AC AAR10764;
XX
DT 22-APR-1991 (first entry)
XX
DE Yeast peptidyl-prolyl cis-trans isomerase.
XX
KW peptidyl-prolyl cis-trans isomerase; PPIase; protein folding.
XX
OS Saccharomyces cerevisiae.
XX
PN EP413440-A.
XX
PD 20-FEB-1991.
XX
PF 19-JUL-1990; 90EP-0307914.
XX
PR 29-DEC-1989; 89JP-0344705.
PR 19-JUL-1989; 89JP-0184738.
PR 06-OCT-1989; 89JP-0260244.
XX
PA (TOFU) TONEN CORP.
XX
PI Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
XX
DR WPI: 1991-052736/08.
DR N-PSDB; AAQ10546.

XX New peptidyl-prolyl cis-trans isomerase(s) from yeast and E.coli
PT - used to accelerate protein folding
XX
PS Claim 2; Fig 7; 53pp; English.
XX
CC The yeast PPIase has the following properties: 1. it isomerises an
CC X-Pro bond in a peptide chain (X = any amino acid); 2. it has
CC single molecular weight about 17,000 (by SDS-PAGE); 3. it has
CC single isoelectric point about 5.2 (by iso-electric focussing) and
CC 4. it is inhibited by cyclosporin A. The enzyme is useful for
CC accelerating protein folding, especially for activating
CC recombinantly produced proteins. The PPIase can be produced in the
CC same cell as the recombinant proteins.
CC See also AAQ10542-5 and AAR10762.
XX
SQ Sequence 162 AA;

Query Match 96.0%; Score 48; DB 12; Length 162;
Best Local Similarity 88.9%; Pred. No: 0.39;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFMIQGGDF 9
| | | | | | | | |

Search completed: January 15, 2002, 13:05:27
Job time: 198 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:00:24 ; Search time 37.64 Seconds
(without alignments)
5.381 Million cell updates/sec

Title: US-09-720-469-1
Perfect score: 49
Sequence: 1 KFHVRKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	126	2	US-08-482-728A-10
2	49	100.0	126	2	US-08-482-728A-11
3	49	100.0	208	1	US-08-142-897-7
4	44	89.8	212	1	US-08-142-897-5
5	41	83.7	123	2	US-08-482-728A-6
6	41	83.7	523	2	US-08-482-728A-19
7	41	83.7	523	4	US-09-028-366-4
8	40	81.6	527	4	US-09-028-366-2
9	40	81.6	527	4	US-09-028-366-3
10	39	79.6	176	1	US-08-145-995A-3
11	39	79.6	176	2	US-08-451-747-3
12	39	79.6	176	3	US-09-134-852-3
13	39	79.6	269	4	US-09-028-366-6
14	39	79.6	591	1	US-08-145-995A-21
15	39	79.6	591	2	US-08-451-747-21
16	39	79.6	591	3	US-09-134-852-21
17	38	77.6	126	2	US-08-482-728A-16
18	38	77.6	134	2	US-08-482-728A-14
19	38	77.6	162	1	US-08-142-897-9
20	38	77.6	162	1	US-08-145-995A-14
21	38	77.6	162	2	US-08-451-747-14
22	38	77.6	162	3	US-09-134-852-14
23	38	77.6	171	4	US-09-028-366-7
24	38	77.6	176	1	US-08-145-995A-4
25	38	77.6	176	2	US-08-451-747-4
26	38	77.6	176	3	US-09-134-852-4
27	38	77.6	3224	2	US-08-705-660-34

28	38	77.6	3224	3	US-08-989-045-34	Sequence 34, Appl
29	37	75.5	123	2	US-08-482-728A-7	Sequence 7, Appl
30	37	75.5	147	3	US-09-136-442-3	Sequence 3, Appl
31	36	73.5	123	2	US-08-482-728A-8	Sequence 8, Appl
32	36	73.5	134	2	US-08-482-728A-13	Sequence 13, Appl
33	36	73.5	148	1	US-08-145-995A-6	Sequence 6, Appl
34	36	73.5	148	2	US-08-451-747-6	Sequence 6, Appl
35	36	73.5	148	3	US-09-134-852-6	Sequence 6, Appl
36	36	73.5	175	1	US-08-145-995A-5	Sequence 5, Appl
37	36	73.5	175	2	US-08-451-747-5	Sequence 5, Appl
38	36	73.5	175	3	US-09-134-852-5	Sequence 5, Appl
39	35	71.4	161	1	US-08-145-995A-13	Sequence 13, Appl
40	35	71.4	161	2	US-08-451-747-13	Sequence 13, Appl
41	35	71.4	161	3	US-09-134-852-13	Sequence 13, Appl
42	35	71.4	2232	4	US-09-091-219-25	Sequence 25, Appl
43	35	71.4	2247	4	US-09-091-219-2	Sequence 2, Appl
44	33	67.3	28	3	US-08-486-099-88	Sequence 88, Appl
45	33	67.3	28	3	US-08-360-107A-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-08-482-728A-10
; Sequence 10, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-482-728A-10

Query Match 100.0% Score 49; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFHVRKDF 9

Db 35 KHRVVKDF 43

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US-08-482-728A-11

RESULT 2

US-08-482-728A-11, Application US/08482728A

Sequence 11, Patent No. 5968802

GENERAL INFORMATION:

APPLICANT: Wang, Bruce

APPLICANT: Fisher, Joseph

APPLICANT: Pavan, Donald

TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobbach, Test, Albritton

ADDRESSEE: & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482.728A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Silva, Robin M.

REGISTRATION NUMBER: 38,304

REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-482-728A-11

Query Match 100.0%; Score 49; DB 2; Length 126;

Best Local Similarity 100.0%; Pred. No. 0.023;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHRVVKDF 9

Db 35 KHRVVKDF 43

|||||

US-08-142-897-7

RESULT 3

US-08-142-897-7

Sequence 7, Application US/08142897

Patent No. 5447852

GENERAL INFORMATION:

APPLICANT: Friedman, Jeffrey S.

APPLICANT: Weissman, Irving L.

TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Tracy J. Dunn

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/142,897

FILING DATE: 05-AUG-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/005,917

FILING DATE: 15-JAN-1993

PRIOR APPLICATION DATA:

US-08-142-897-7

Query Match 100.0%; Score 49; DB 1; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHRVVKDF 9

Db 84 KHRVVKDF 92

|||||

US-08-142-897-5

RESULT 4

US-08-142-897-5

Sequence 5, Application US/08142897

Patent No. 5447852

GENERAL INFORMATION:

APPLICANT: Friedman, Jeffrey S.

APPLICANT: Weissman, Irving L.

TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Tracy J. Dunn

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/142,897

FILING DATE: 05-AUG-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/005,917

FILING DATE: 15-JAN-1993

PRIOR APPLICATION DATA:

US-08-142-897-7

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; APPLICATION NUMBER: US 07/740,375
; FILING DATE: 05-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy D.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 5490A-92-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-142-897-5

Query Match      89.8%; Score 44; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVVKDF 9
Db 87 FHRVVKDF 94

RESULT 5
US-08-482-728A-6
; Sequence 6, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-482-728A-19

Query Match      83.7%; Score 41; DB 2; Length 523;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFHVRVKDF 9
Db 320 KFHRLIKNF 328

RESULT 7
US-09-028-366-4
; Sequence 4, Application US/09028366
; Patent No. 6150501
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: HONG, XIQIANG
; APPLICANT: MA, DONG
; TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING
; CYCLOPHILIN AND RELATED METHODS
; NUMBER OF SEQUENCES: 16
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: New England Biolabs, Inc.
;; STREET: 32 Tozer Road
;; CITY: Beverly
;; STATE: MA
;; COUNTRY: US
;; ZIP: 01915
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/028,366
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Williams, Gregory D
;; REGISTRATION NUMBER: 30901
;; REFERENCE/DOCKET NUMBER: NEB-133
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 978-927-5054
;; TELEFAX: 978-927-1705
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 523 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: linear
;; TOPOLOGY: protein
;; MOLECULE TYPE: protein
US-09-028-366-4

Query Match 83.7%; Score 41; DB 4; Length 523;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHVRVKDF 9
Db 320 KFHRLIKNF 328

RESULT 8
US-09-028-366-2
; Sequence 2, Application US/09028366
; Patent No. 6150501
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: HONG, XIQIANG
; APPLICANT: MA, DONG
; TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING
; TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: New England Biolabs, Inc.
; STREET: 32 Tozer Road
; CITY: Beverly
; STATE: MA
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,366
; FILING DATE:
; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Williams, Gregory D
;; REGISTRATION NUMBER: 30901
;; REFERENCE/DOCKET NUMBER: NEB-133
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 978-927-5054
;; TELEFAX: 978-927-1705
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 527 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: internal
US-09-028-366-2

Query Match 81.6%; Score 40; DB 4; Length 527;
Best Local Similarity 66.7%; Pred. No. 4.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHVRVKDF 9
Db 321 KFHRLIKNF 329

RESULT 9
US-09-028-366-3
; Sequence 3, Application US/09028366
; Patent No. 6150501
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: HONG, XIQIANG
; APPLICANT: MA, DONG
; TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING
; TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: New England Biolabs, Inc.
; STREET: 32 Tozer Road
; CITY: Beverly
; STATE: MA
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,366
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 978-927-5054
; TELEFAX: 978-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 527 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-028-366-3

Query Match      81.6%; Score 40; DB 4; Length 527;
Best Local Similarity 66.7%; Pred. No. 4.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHRVIKDF 9
Db 321 KHRRIIRNF 329

RESULT 10
US-08-145-995A-3
; Sequence 3, Application US/08145995A
; Patent No. 5482850
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS, NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,747
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,995
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-046-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-451-747-3

Query Match      79.6%; Score 39; DB 2; Length 176;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIKDF 9
Db 64 FHRVIKNF 71

RESULT 12
US-09-134-852-3
; Sequence 3, Application US/09134852
; Patent No. 6127148
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,852
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,995
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-134-852-3

Query Match 79.6%; Score 39; DB 3; Length 176;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHVRVKDF 9
| | | | | | |
Db 64 FHVRVKNF 71

RESULT 13
US-09-028-366-6
; Sequence 6, Application US/09028366
; Patent No. 6150501
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: HONG, XIQIANG
; APPLICANT: MA, DONG
; TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING
; TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: New England Biolabs, Inc.
; STREET: 32 Tozer Road
; CITY: Beverly
; STATE: MA
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,366
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 978-927-5054

; TELEFAX: 978-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-028-366-6

Query Match 79.6%; Score 39; DB 4; Length 269;
Best Local Similarity 87.5%; Pred. No. 3.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHVRVKDF 9
| | | | | | |
Db 64 FHVRVKNF 71

RESULT 14
US-08-145-995A-21
; Sequence 21, Application US/08145995A
; Patent No. 5482850
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,995A
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-145-995A-21

Query Match 79.6%; Score 39; DB 1; Length 591;
Best Local Similarity 87.5%; Pred. No. 7.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHVRVKDF 9
| | | | | | |
Db 66 FHVRVKNF 73

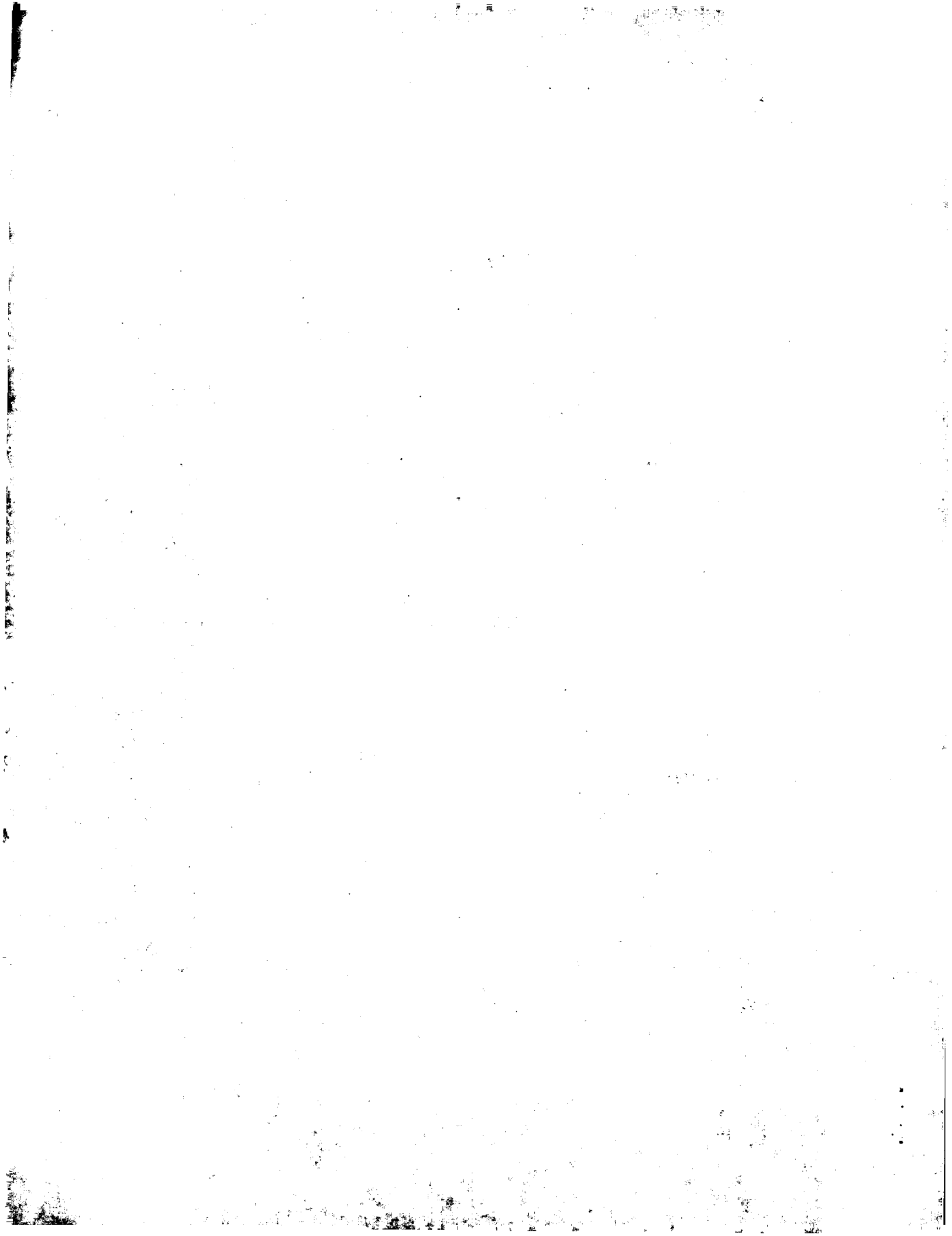
Tue Jan 15 13:46:27 2002

RESULT 15
US-08-451-747-21
; Sequence 21, Application US/08451747
; Patent No. 5821107
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,747
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,995
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-046-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-451-747-21

Query Match 79.6%; Score 39; DB 2; Length 591;
Best Local Similarity 87.5%; Pred No. 7.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVKNDF 9
| | | | | | | |
Db 66 FHRVKNF 73

Search completed: January 15, 2002, 13:03:58
Job time: 214 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2002, 13:02:29 ; Search time 42.04 seconds
(without alignments)
16.308 Million cell updates/sec

Title: US-09-720-469-1

Perfect score: 49

Sequence: 1 KFHVRVVKDF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	183	2 S71547	peptidylprolyl iso
2	49	100.0	207	2 A40516	peptidylprolyl iso
3	49	100.0	208	1 CSHUB	peptidylprolyl iso
4	49	100.0	212	2 A54204	peptidylprolyl iso
5	49	100.0	216	2 A56861	peptidylprolyl iso
6	45	91.8	199	2 F84808	probable peptidyl-
7	44	89.8	183	2 T18578	peptidylprolyl iso
8	44	89.8	212	2 A40047	peptidylprolyl iso
9	44	89.8	215	2 A71261	peptidylprolyl iso
10	44	89.8	371	2 S48567	peptidylprolyl iso
11	43	87.8	196	2 E86736	cyclophilin-like p
12	43	87.8	204	2 T21587	peptidyl-prolyl ci
13	43	87.8	260	2 B53422	peptidylprolyl iso
14	43	87.8	754	1 JC5314	peptidylprolyl iso
15	42	85.7	164	2 C84777	CD28/cdc2-like ki
16	41	83.7	356	2 S62327	cyclophilin-like p
17	41	83.7	523	2 T23003	probable 40 kd pep
18	40	81.6	201	2 T18573	hypothetical prote
19	39	79.6	404	2 D84533	hypothetical prote
20	38	77.6	141	2 H69044	peptidylprolyl iso
21	38	77.6	155	2 T38930	peptidylprolyl iso
22	38	77.6	162	1 CSBY	peptidylprolyl iso
23	38	77.6	165	2 S28020	peptidylprolyl iso
24	38	77.6	171	2 S74880	peptidylprolyl iso
25	38	77.6	171	2 T27371	peptidylprolyl iso
26	38	77.6	172	2 T27882	peptidylprolyl iso
27	38	77.6	172	2 T06073	peptidylprolyl iso
28	38	77.6	192	2 T27034	peptidylprolyl iso
29	38	77.6	393	2 S57050	cyclophilin-like p

ALIGNMENTS

RESULT 1

S71547

peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat

N:Alternate names: cyclophilin B; PPIASE

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999

C:Accession: S71547

R:Ruecknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaefer, M.; Fischer, G.

submitted to the Protein Sequence Database, November 1996

A:Reference number: S71547

A:Accession: S71547

A:Molecule type: protein

A:Residues: 1-183 <RUE>

A:Experimental source: liver

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase

F:1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <MAT>

F:10-172/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 49; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.021; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 KFHVRVVKDF 9

Db 59 KFHVRVVKDF 67

RESULT 2

A40516

peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999

C:Accession: A40516

R:Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.

J. Biol. Chem. 266, 10739-10742, 1991

A:Title: S-cyclophilin. New member of the cyclophilin family associated with the secr

A:Reference number: A40516; MUID:91250364

A:Accession: A40516

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-207 <CAR>

A:Cross-references: GB:M63553; NID:g212648; PIDN:AAA9064.1; PID:g212649

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase; cyclosporin A binding

F:34-196/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 49; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.024; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

probable cyclophilin
hypothetical prote
natural killer cel
natural killer cel
TMV resistance pro
Ran-binding protei
peptidylprolyl iso
peptidylprolyl iso
peptidylprolyl iso
peptidylprolyl iso
peptidylprolyl iso
peptidylprolyl iso
cyclophilin isofo
cyclophilin-like p
hypothetical prote

QY 1 KFHVRVVKDF 9
 |||||
 Db 83 KFHVRVVKDF 91

RESULT 3
 CSHUB

peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human
 N;Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin
 C;Species: Homo sapiens (man)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000
 C;Accession: A39118; A39722; A40515; S65742
 R;Price, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991
 A;Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl isomerase
 A;Reference number: A39118; MUID:91156714
 A;Accession: A39118
 A;Molecule type: mRNA
 A;Residues: 1-208 <PRI>
 A;Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335
 R;Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
 Mol. Cell. Biol. 11, 3484-3491, 1991
 A;Title: An endoplasmic reticulum-specific cyclophilin.
 A;Reference number: A39722; MUID:91260697
 A;Accession: A39722
 A;Molecule type: mRNA
 A;Residues: 1-208 <HAS>
 A;Cross-references: GB:M60457; NID:g181249; PIDN:AAA35733.1; PID:g181250
 R;Spik, G.; Haendler, B.; Delmas, O.; Mariller, C.; Chamoux, M.; Maes, P.; Tartar, A.; M
 J. Biol. Chem. 266, 10735-10738, 1991
 A;Title: A novel secreted cyclophilin-like protein (SCYLP).
 A;Reference number: A40515; MUID:91250363
 A;Accession: A40515
 A;Molecule type: mRNA
 A;Residues: 'MLRUSERN', 1-208 <SPI>
 A;Cross-references: GB:M63573; NID:g337998; PIDN:AAA36601.1; PID:g337999
 A;Note: the authors' translation begins at an ATG codon in poor context for initiation
 A;Note: parts of this sequence, including the amino end of the mature form, were confir
 R;Mariller, C.; Allain, F.; Kouach, M.; Spik, G.
 Biochim. Biophys. Acta 1293, 31-38, 1996
 A;Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated form
 A;Reference number: S65742; MUID:96186273
 A;Accession: S65742
 A;Molecule type: protein
 A;Residues: 26-30;203 <MAR>
 A;Experimental source: milk
 C;Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence
 C;Genetics:
 A;Gene: GDB:PPIB
 A;Cross-references: GDB:127610; OMIM:123841
 A;Map position: 15q21-15q22
 C;Function:
 A;Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
 C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C;Keywords: cis-trans-isomerase; cyclosporin A binding; glycoprotein; T-cell
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-203/Product: peptidylprolyl isomerase B #status experimental <MAT>
 F:35-197/Domain: cyclophilin homology <CYP>
 F:140/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 49; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFHVRVVKDF 9
 |||||
 Db 84 KFHVRVVKDF 92

RESULT 4

A54204
 peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human
 N;Alternate names: cyclophilin C
 C;Species: Homo sapiens (man)
 C;Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
 C;Accession: A54204
 R;Schneider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurlo, M.G.; Quesn
 Biochemistry 33, 8218-8224, 1994
 A;Title: Human cyclophilin C: primary structure, tissue distribution, and determinati
 A;Reference number: A54204; MUID:94304830
 A;Accession: A54204
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-212 <SCH>
 A;Cross-references: GB:S71018; NID:g547303; PIDN:AA31350.1; PID:g547304
 A;Experimental source: kidney
 A;Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBI:P:149388)
 C;Genetics:
 A;Gene: GDB:PPIC
 A;Cross-references: GDB:136196; OMIM:123842
 A;Map position: 15q21-15q22
 C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C;Keywords: cis-trans-isomerase; cyclosporin A binding
 F:37-199/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 49; DB 2; Length 212;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFHVRVVKDF 9
 |||||
 Db 86 KFHVRVVKDF 94

RESULT 5

A56861
 peptidylprolyl isomerase (EC 5.2.1.8) Cyp-SI precursor - mouse
 N;Alternate names: cyclophilin B; cyclophilin-SI; cyclosporin A-binding protein
 C;Species: Mus musculus (house mouse)
 C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
 C;Accession: A56861; B39722; S21835
 R;Schumacher, A.; Schroter, H.; Muthaupt, G.; Nordheim, A.
 Biochim. Biophys. Acta 1129, 13-22, 1991
 A;Title: Murine cyclophilin-SI: a variant peptidyl-prolyl isomerase with a putative s
 A;Reference number: A56861; MUID:92096454
 A;Accession: A56861
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-216 <SCH>
 A;Experimental source: teratocarcinoma F9 cells
 A;Note: sequence extracted from NCBI backbone (NCBIN:73234, NCBI:P:73239)
 A;Note: parts of this sequence, including the amino end of the mature protein, were c
 R;Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
 Mol. Cell. Biol. 11, 3484-3491, 1991
 A;Title: An endoplasmic reticulum-specific cyclophilin.
 A;Reference number: A39722; MUID:91260697
 A;Accession: B39722
 A;Molecule type: mRNA
 A;Residues: 9-216 <HAS>
 A;Cross-references: GB:M60456; NID:g192864; PIDN:AAA37498.1; PID:g192865
 R;Nordheim, A.
 submitted to the EMBL Data Library, May 1991
 A;Reference number: S21835
 A;Accession: S21835
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 9-216 <NOR>
 A;Cross-references: EMBL:X58990; NID:g53034; PIDN:CAA41736.1; PID:g53035
 C;Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
 C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C;Keywords: Cis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
 F:1-33/Domain: signal sequence #status predicted <SIG>

F:34-216/Product: peptidylprolyl isomerase B #status predicted <MAT>
F:43-205/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 49; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFRVIRKDF 9
|||||

Db 92 KFRVIRKDF 100

RESULT 6

F84808
probable peptidyl-prolyl cis-trans isomerase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: F84808
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: F84808
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199 <STO>
A:Cross-references: GB:AE002093; NID:g3785999; PIDN:AAC67345.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g38730
A:Map position: 2
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

Query Match 91.8%; Score 45; DB 2; Length 199;
Best Local Similarity 88.9%; Pred. No. 0.14;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFRVIRKDF 9
:|||||

Db 85 QFRVIRKDF 93

RESULT 7

T18578
peptidylprolyl isomerase (EC 5.2.1.8) cyp-11 [similarity] - Caenorhabditis elegans
N:Contains: cyclophilin
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C:Accession: T18578; T24269
R:Page, A.P.; MacNiven, K.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z18986
A:Accession: T18578
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-183 <PAG>
A:Cross-references: EMBL:U34955; PIDN:AAC47115.1
A:Experimental source: strain Bristol N2
R:Sims, M.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19867
A:Accession: T24269
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-183 <WIL>
A:Cross-references: EMBL:Z66499; PIDN:CAA91297.1; GSPDB:GN00020; CESP:T01B7.4
A:Experimental source: clone T01B7
C:Genetics:
A:Gene: CESP:cyp-11
A:Map position: 2

A:Introns: 34/3; 87/3; 148/1
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:16-183/Domain: cyclophilin homology <CYP>

Query Match 89.8%; Score 44; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIRKDF 9
|||||

Db 71 FHRVIRKDF 78

RESULT 8

A40047
peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin C) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: A40047
R:Friedman, J.; Weissman, I.
Cell 66, 799-806, 1991
A:Title: Two cytoplasmic candidates for immunophilin action are revealed by affinity
A:Reference number: A40047; MUID:91347379
A:Accession: A40047
A:Molecule type: DNA
A:Residues: 1-212 <PRI>
A:Cross-references: GB:M74227; NID:g192898; PIDN:AAA37511.1; PID:g192899
C:Comment: This protein binds the immunosuppressive drug cyclosporin A.
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F:37-199/Domain: cyclophilin homology <CYP>

Query Match 89.8%; Score 44; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIRKDF 9
|||||

Db 87 FHRVIRKDF 94

RESULT 9

A71261
peptidylprolyl isomerase (EC 5.2.1.8) TP0947 [similarity] - syphilis spirochete
N:Contains: cyclophilin
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 08-Sep-2000
C:Accession: A71261
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770
A:Accession: A71261
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-215 <COL>
A:Cross-references: GB:AE001263; GB:AE000520; NID:g3323266; PIDN:AAC65904.1; PID:g332
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0947
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:34-206/Domain: cyclophilin homology <CYP>

Query Match 89.8%; Score 44; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIKDF 9
|||||
Db 89 FHRVIKDF 96

RESULT 10

S48567
N: peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans
N: Contains: cyclophilin
C: Species: Saccharomyces cerevisiae
C: Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 24-Sep-1999
C: Accession: S48567; S71742
R: Pauley, A.
submitted to the EMBL Data Library, September 1994
A: Description: The sequence of S. cerevisiae cosmid 8167.
A: Reference number: S48545
A: Accession: S48567
A: Molecule type: DNA
A: Residues: 1-371 <PAU>
A: Cross-references: EMBL:U14913; NID:g544497; PIDN:AAB67445.1; PID:g544520; MIPS:YLR216C
R: Duina, A.A.; Marsh, J.A.; Gaber, R.F.
Yeast 12, 943-952, 1996
A: Title: Identification of two Cyp-40-like cyclophilins in Saccharomyces cerevisiae, and
A: Reference number: S71742; MUID:97027304
A: Accession: S71742
A: Status: nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 1-371 <DU1>
A: Cross-references: EMBL:U48867; NID:g1515347; PIDN:AAC49414.1; PID:g1515348
C: Genetics:
A: Gene: SGD:CPR6; CYP40
A: Cross-references: SGD:S0004206; MIPS:YLR216C
A: Map position: 12R
C: Superfamily: peptidylprolyl isomerase Cyp-40; cyclophilin homology
C: Keywords: cytosol; heat shock; stress-induced protein
F: 3-175/Domain: cyclophilin homology <CYP>

Query Match 89.8%; Score 44; DB 2; Length 371;

Best Local Similarity 100.0%; Pred. No. 0.43; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIKDF 9
|||||
Db 62 FHRVIKDF 69

RESULT 11

E86736
N: peptidylprolyl cis-trans isomerase [imported] - Lactococcus lactis subsp. lactis (strain
C: Species: Lactococcus lactis subsp. lactis
C: Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C: Accession: E86736
R: Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. in press, 2001
A: Title: The complete genome sequence of the lactic acid bacterium.
A: Reference number: A86625
A: Accession: E86736
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-196 <STO>
A: Cross-references: GB:AE005176; NID:g12723824; PIDN:AAK04991.1; GSPDB:GN00146
A: Experimental source: strain IL1403
C: Genetics:
A: Gene: pp18
C: Superfamily: peptidylprolyl isomerase; cyclophilin homology

Query Match 87.8%; Score 43; DB 2; Length 196;

Best Local Similarity 87.5%; Pred. No. 0.35; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVIKDF 9
|||||
Db 55 FHRVIKDF 62

RESULT 12

T21587
N: peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans
N: Contains: cyclophilin
C: Species: Caenorhabditis elegans
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C: Accession: T21587
R: Cottage, A.
submitted to the EMBL Data Library, March 1997
A: Reference number: Z19446
A: Accession: T21587
A: Status: preliminary; translated from GB/EMBL/DBDJ
A: Molecule type: DNA
A: Residues: 1-204 <WIL>
A: Cross-references: EMBL:Z92784; PIDN:CAH07192.1; GSPDB:GN00019; CESP:F31C3.1
A: Experimental source: clone F31C3
C: Genetics:
A: Gene: CESP:F31C3.1
A: Map position: 1
A: Introns: 69/3
C: Superfamily: peptidylprolyl isomerase; cyclophilin homology
C: Keywords: cis-trans-isomerase
F: 28-190/Domain: cyclophilin homology <CYP>

Query Match 87.8%; Score 43; DB 2; Length 204;

Best Local Similarity 88.9%; Pred. No. 0.36; Mismatches 8; Conservative 0; Indels 1; Gaps 0;

QY 1 KFHRIKDF 9
|||||
Db 77 KFHRIKDF 85

RESULT 13

B53422
N: peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana
N: Alternate names: cyclophilin homolog ROC4; protein F21F14.200
C: Species: Arabidopsis thaliana (mouse-ear cress)
C: Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 19-May-2000
C: Accession: B53422; T47995
R: Lippuner, V.; Chou, I.T.; Scott, S.V.; Ettinger, W.F.; Theg, S.M.; Gasser, C.S.
J. Biol. Chem. 269, 7863-7868, 1994
A: Title: Cloning and characterization of chloroplast and cytosolic forms of cyclophilin
A: Reference number: A53422; MUID:94179146
A: Accession: B53422
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-260 <LIP>
A: Cross-references: GB:LJ4845; NID:g405130; PIDN:AAA20048.1; PID:g405131
R: Choinsne, N.; Robert, C.; Bröttier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.;
submitted to the Protein Sequence Database, February 2000
A: Reference number: Z24481
A: Accession: T47995
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-260 <CHO>
A: Cross-references: EMBL:AL138642
A: Experimental source: cultivar Columbia; BAC clone F21F14
C: Genetics:
A: Gene: ROC4
A: Map position: 3
A: Introns: 18/3; 81/3; 133/1; 162/3; 181/1; 209/3
A: Note: F21F14.200
C: Superfamily: peptidylprolyl isomerase; cyclophilin homology
C: Keywords: cis-trans-isomerase; cyclosporin A binding
F: 94-256/Domain: cyclophilin homology <CYP>

Query Match 87.8%; Score 43; DB 2; Length 260;
Best Local Similarity 87.5%; Pred. No. 0.47;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVVKDF 9
| | | : | | | |
Db 144 FHRVVKDF 151

RESULT 14

JC5314
CDC28/cdc2-like kinase associating arginine-serine cyclophilin - human
N:Alternate names: CARS-Cyp
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: JC5314; G02262
R:Nestel, P.P.; Colwall, K.; Harper, S.; Pawson, T.; Anderson, S.K.
Gene 180, 151-155, 1996
A:Title: RS cyclophilins: Identification of an NK-TL-related cyclophilin.
A:Reference number: JC5314; MUID:97128820
A:Accession: JC5314
A:Molecule type: mRNA
A:Residues: 1-754 <NES>
A:Cross-references: EMBL:U40763; MID:g1117967; PIDN:AAB40347.1; PID:g1117968
A:Experimental source: thymus
A:Note: submitted to the EMBL Data Library, November 1995
C:Comment: This protein contains a cyclophilin-related domain, two 140K nuclear phospho-
splicing by binding to splicing factors containing serine-arginine repeats protein.
C:Genetics:
A:Gene: GDB:CYP; CARS-CYP
A:Cross-references: GDB:9956062
C:Superfamily: CARS cyclophilin; cyclophilin homology
F:7-177/Domain: cyclophilin homology <Cyp>

Query Match 87.8%; Score 43; DB 1; Length 754;
Best Local Similarity 87.5%; Pred. No. 1.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVVKDF 9
| | | : | | | |
Db 65 FHRVVKDF 72

RESULT 15

C84777
cyclophilin-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: C84777
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: C84777
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-164 <STO>
A:Cross-references: GB:AE002093; NID:g4678225; PIDN:AAD26970.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g36130
A:Map position: 2
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

Query Match 85.7%; Score 42; DB 2; Length 164;
Best Local Similarity 75.0%; Pred. No. 0.46;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVVKDF 9

Db 51 FHRVVKDF 58
| | | : | | | |

Search completed: January 15, 2002, 13:06:15
Job time: 226 sec

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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:04:04 ; Search time 24.88 Seconds
(without alignments)
13.263 Million cell updates/sec

Title: US-09-720-469-1
Perfect score: 49
Sequence: 1 KFHRIKDF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	49	100.0	207	1 CYPB_CHICK	P24367 gallus gall
2	49	100.0	208	1 CYPB_BOVIN	P80311 bos taurus
3	49	100.0	208	1 CYPB_HUMAN	P23284 homo sapien
4	49	100.0	208	1 CYPB_MOUSE	P24369 mus musculus
5	49	100.0	212	1 CYPB_HUMAN	P45877 homo sapien
6	44	89.8	183	1 CYPB_CAEEL	P52018 caenorhabdi
7	44	89.8	212	1 CYPB_MOUSE	P50412 mus musculus
8	44	89.8	215	1 PPIB_TREPA	O86105 treponema p
9	44	89.8	371	1 CYP6_YEAST	P53691 saccharomyc
10	43	87.8	204	1 CYP5_CAEEL	P52013 caenorhabdi
11	43	87.8	260	1 CYP4_ARATH	P34791 arabidopsis
12	41	83.7	208	1 CYPB_RAT	P24368 rattus norv
13	41	83.7	523	1 CYP4_CAEEL	P52012 caenorhabdi
14	40	81.6	201	1 CYP6_CAEEL	P52014 caenorhabdi
15	39	79.6	843	1 CYP1_BRUMA	P27450 brugia mala
16	38	77.6	155	1 CYP2_SCHPO	P87051 schizosacch
17	38	77.6	161	1 CYPH_YEAST	P14832 saccharomyc
18	38	77.6	163	1 CYPH_UROFA	O00060 uromyces fa
19	38	77.6	165	1 PPL_STRCH	Q06118 streptomyce
20	38	77.6	171	1 CYP2_CAEEL	P52010 caenorhabdi
21	38	77.6	171	1 CYP7_CAEEL	P52015 caenorhabdi
22	38	77.6	172	1 CYP1_ARATH	P34790 arabidopsis
23	38	77.6	192	1 CYP1_CAEEL	P52009 caenorhabdi
24	38	77.6	393	1 CYP7_YEAST	P47103 saccharomyc
25	38	77.6	1085	1 RBP2_BOVIN	P48820 bos taurus
26	38	77.6	1453	1 NKCR_MOUSE	P30415 mus musculus
27	38	77.6	1462	1 NKCR_HUMAN	P30414 homo sapien
28	38	77.6	3224	1 RBP2_HUMAN	P49792 homo sapien
29	37	75.5	147	1 CYP4_CAEEL	P52011 caenorhabdi
30	37	75.5	173	1 CYP3_CAEEL	P52011 caenorhabdi
31	37	75.5	182	1 CYPC_YEAST	P25719 saccharomyc
32	37	75.5	466	1 CYP8_CAEEL	P25016 caenorhabdi
33	36	73.5	309	1 CYP9_CAEEL	Q09637 caenorhabdi

34	36	73.5	370	1 CYP4_BOVIN	P25882 bos taurus
35	36	73.5	370	1 CYP4_HUMAN	Q08752 homo sapien
36	35	71.4	161	1 CYPH_ECHGR	P14088 echinococcu
37	35	71.4	164	1 CYPH_BLAGR	P54985 biatella g
38	35	71.4	385	1 TP6A_AERPE	O9ye67 aeropyrum p
39	34	69.4	172	1 CYPH_MAIZE	P21569 zea mays (m
40	34	69.4	300	1 CYPE_DROME	O93933 drosophilla
41	34	69.4	869	1 PEMI_YEAST	P03374 saccharomyc
42	33	67.3	165	1 CYPH_DROME	P25007 drosophilla
43	33	67.3	172	1 CYPH_LUPLU	O49886 lupinus lut
44	33	67.3	182	1 PPIA_MYCTU	P71578 mycobacteri
45	33	67.3	188	1 PPIA_ACICA	P42693 acinetobact

ALIGNMENTS

RESULT 1
CYPB_CHICK
ID CYPB_CHICK STANDARD; PRT: 207 AA.
AC P24367;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91250364; PubMed=2040593;
RA Caroni P., Rothenfluh A., McGlynn E., Schneider C.;
RT "S-cyclophilin. New member of the cyclophilin family associated with
the secretory pathway.";
RL J. Biol. Chem. 266:10739-10742(1991).
CC -!- FUNCTION: PIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PIASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC
CC EMBL; M63553; AAA49064.1; .
DR PIR: A40516; A40516.
DR HSP: P23284; LCYN.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro-isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
Multigene family.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 207 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 198 207 PREVENT SECRETION FROM ER
(BY SIMILARITY).
SQ SEQUENCE 207 AA; 22413 MW; D9C0C2E528E25B59 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KHRVIRKDF 9
Db 83 KHRVIRKDF 91

RESULT 2
CYPB_BOVIN
ID CYPB_BOVIN STANDARD; PRT; 208 AA.
AC P80311;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
GN PPIB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Carrello A., Mark P.J., House A.K., Ratajczak T.;
RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 26-71.
RC TISSUE=Brain;
RA Gallat A., Bouet F.;
RL "Cyclophilin-B is an abundant protein whose conformation is similar
to cyclophilin-A."
RN [3]
RP FERS Lett. 347:31-36(1994).
RN [3]
RP SEQUENCE OF 26-45.
RA MEDLINE=94280416; PubMed=8010972;
RA Bose S., Muecke M., Freedman R.B.;
RT "The characterization of a cyclophilin-type peptidyl prolyl
cis-trans-isomerase from the endoplasmic-reticulum lumen."
RN Biochem. J. 300:871-875(1994).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
-----
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-----
DR EMBL: D14073; BAA03158.1; -.
DR HSSP: P23284; 1CVN.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; isomerase; Rotamase; Signal; Endoplasmic reticulum;
Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER.
FT CONFLICT 30 30 K -> G (IN REF. 3).
SQ SEQUENCE 208 AA; 22701 MW; 0097C88289AF6276 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHRVIRKDF 9
Db 84 KHRVIRKDF 92

RESULT 3
CYPB_HUMAN
ID CYPB_HUMAN STANDARD; PRT; 208 AA.
AC P23284;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
GN PPIB OR CYPB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-40.
RA MEDLINE=91156714; PubMed=2000394;
RA Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,
Walsh C.T.;
RT "Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-
prolyl isomerase with a signal sequence."
RN Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=91250363; PubMed=2040592;
RA Spik G., Haendler B., Delmas O., Mariller C., Chamoux M., Maes P.,
Tartar A., Montreuil J., Stedman K., Kocher H.P., Keller R.,
Hiestand P.C., Movva N.R.;
RT "A novel secreted cyclophilin-like protein (SCYLP)."
RN J. Biol. Chem. 266:10735-10738(1991).
RN [3]
RP SEQUENCE OF 2-208 FROM N.A.
RA MEDLINE=91260697; PubMed=1710767;
RA Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
RT "An endoplasmic reticulum-specific cyclophilin."
RN Mol. Cell. Biol. 11:3484-3491(1991).
RN [4]
RP SEQUENCE OF 64-76 AND 151-157.
RA MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puyte M., Gesser B., Celis J.E.,
Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes."
RN Electrophoresis 13:960-969(1992).
RN [5]
RP SUBCELLULAR LOCATION.
RA MEDLINE=92112948; PubMed=1530944;
RA Arber S., Krause K.H., Caroni P.;
RT "S-cyclophilin is retained intracellularly via a unique COOH-terminal
sequence and colocalizes with the calcium storage protein
calreticulin."
RN J. Cell Biol. 116:113-125(1992).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RA MEDLINE=94255495; PubMed=8197205;
RA Mikol V., Kallen J., Walkinshaw M.D.;
RT "X-ray structure of a cyclophilin B/cyclosporin complex: comparison
with cyclophilin A and delineation of its calcineurin-binding
domain."
RN Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).
RN [7]
RT FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
```

CC CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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CC CC -----

DR EMBL: M60857; AAA52150.1; -

DR EMBL: M63573; AAA36601.1; AUT_INIT.

DR EMBL: M60457; AAA35733.1; -

DR PIR: A39118; CSHUB.

DR PIR: A40515; A40515.

DR PDB: 1CYN; 29-JAN-96.

DR AARhus/Ghent-2DPAGE; 117; NEPHGE.

DR MIM; 123841; -

DR InterPro: IPR002130; CSA_PPIase.

DR Pfam; PF00160; pro_isomerase; 1.

DR PRINTS; PR00153; CSAPPISMRASE.

DR PROSITE; PS00170; CSA_PPIASE.1; 1.

DR PROSITE; PS50072; CSA_PPIASE.2; 1.

DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;

KW Multigene family; 3D-structure.

FT SIGNAL 1 25

FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.

FT SITE 199 208 PREVENT SECRETION FROM ER.

FT SITE 208 AA; 22742 MW; A814481B7EBD4579 CRC64;

SQ SEQUENCE 208 AA; 22742 MW; A814481B7EBD4579 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFHVRVVKDF 9

Db 84 KFHVRVVKDF 92

RESULT 4

CYPB_MOUSE

ID CYPB_MOUSE STANDARD; PRT; 208 AA.

AC P24369;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)

DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).

GN PP1B.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91260697; PubMed=1710767;

RA Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;

RT "An endoplasmic reticulum-specific cyclophilin.";

RL Mol. Cell. Biol. 11:3484-3491(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX STRAIN=C57BL;

RC MEDLINE=92096454; PubMed=1756174;

RA Schumacher A., Schroeter H., Multhaup G., Nordheim A.;

RT "Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a

RL putative signal sequence expressed in differentiating F9 cells.";

RL Biochim. Biophys. Acta 1129:13-22(1991).

CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

CC PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).

CC CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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CC CC -----

DR EMBL: M60456; AAA37498.1; -

DR EMBL: X58990; CAA41736.1; -

DR PIR: B39722; B39722.

DR PIR: S21835; S21835.

DR HSSP; P23284; ICYN.

DR MGD; MGI:97750; Ppib.

DR InterPro: IPR002130; CSA_PPIase.

DR Pfam; PF00160; pro_isomerase; 1.

DR PRINTS; PR00153; CSAPPISMRASE.

DR PROSITE; PS00170; CSA_PPIASE.1; 1.

DR PROSITE; PS50072; CSA_PPIASE.2; 1.

DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;

KW Multigene family.

FT SIGNAL 1 25

FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.

FT SITE 199 208 PREVENT SECRETION FROM ER

FT SITE 208 AA; 22713 MW; 4B8DF5AE40BAD3A7 CRC64;

SQ SEQUENCE 208 AA; 22713 MW; 4B8DF5AE40BAD3A7 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFHVRVVKDF 9

Db 84 KFHVRVVKDF 92

RESULT 5

CYPC_HUMAN

ID CYPC_HUMAN STANDARD; PRT; 212 AA.

AC P45877;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)

DE (CYCLOPHILIN C).

GN PP1C OR CYPC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94304830; PubMed=8031755;

RA Schneider H., Charara N., Schmitz R., Wehrli S., Mikol V.,

RA Zurini M.G., Quesniaux V.F., Movva N.R.;

RT "Human cyclophilin C: primary structure, tissue distribution, and

RT determination of binding specificity for cyclosporins.";

RL Biochemistry 33:8218-8224(1994).

CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

CC PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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CC -----
DR EMBL: S71018: AAB31350.1; -;
DR HSSP: P05092; 2RMC.
DR MIM: 123842; -;
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
DR Cyclosporin; Isomerase; Rotamase; Multigene family.
KW SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;

Query Match 100.0%; Score 49; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFRVVKDF 9
| | | | | | | |
DB 86 KFRVVKDF 94

RESULT 6
ID CYPB_CAEEL STANDARD; PRT; 183 AA.
AC P52018;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN-11).
GN CYP-11 OR T01B7.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodirinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=96276416; PubMed=8694762;
RA Page A.P., Macniven K., Hengartner M.O.;
RT "Cloning and biochemical characterization of the cyclophilin
RT homologues from the free-living nematode Caenorhabditis elegans.";
RL Biochem. J. 317:179-185(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Sims M.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC EMBL: U34955; AAC47115.1; -;
DR EMBL: 266495; CAA91297.1; -;
DR HSSP: P05092; 3CYS.
DR WormPep: T01B7.4; CE03588.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.

KW Isomerase; Rotamase; Multigene family.
SQ SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;

Query Match 89.8%; Score 44; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVVKDF 9
| | | | | | | |
DB 71 FHRVVKDF 78

RESULT 7
ID CYPC_MOUSE STANDARD; PRT; 212 AA.
AC P30412;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN C).
GN PPIC OR CYPC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91347379; PubMed=1652374;
RA Friedman J., Weissman I.L.;
RT "Two cytoplasmic candidates for immunophilin action are revealed by
RT affinity for a new cyclophilin: one in the presence and one in the
RT absence of CsA.";
RL Cell 66:799-806(1991).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC EMBL: M74227; AAA37511.1; -;
DR PIR: A40047; A40047.
DR HSSP: P05092; 2RMC.
DR MGD; MGI:97751; Ppic.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Multigene family.
SQ SEQUENCE 212 AA; 22794 MW; C99E7AA5D0FA04B6 CRC64;

Query Match 89.8%; Score 44; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVVKDF 9
| | | | | | | |
DB 87 FHRVVKDF 94

RESULT 8

PP1B_TREPA
ID PP1B_TREPA STANDARD; PRT; 215 AA.
AC O66105;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE).
GN PP1B OR PPI OR TP0947.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97461344; PubMed=9317025;
RA Shevchenko D.V., Akis D.R., Robinson E.J., Li M., Shevchenko O.V.,
RA Radolf J.D.;
RT Identification of homologs for thiorodoxin, peptidyl prolyl cis-trans
RT isomerase, and glycerophosphodiester phosphodiesterase in outer
RT membrane fractions from Treponema pallidum, the syphilis spirochete.";
RL Infect. Immun. 65:4179-4189(1997).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.F., Salzberg S., Peterson J.,
RA Khalak L., Richardson B., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald H., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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CC -----
DR EMBL; U97573; AAC08055.1; -;
DR EMBL; AE001263; AAC65904.1; -;
DR TIGR; TP0947; -;
DR InterPro: IPR0021130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; FALSE_NEG.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
DR Isomerase; Rotamase; Complete proteome.
KW Isomerase; Rotamase; Complete proteome.
SQ SEQUENCE 215 AA; 23272 MW; CCAL589C1F5A6D0B CRC64;

Query Match 89.8%; Score 44; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FHRVIKDF 9
Db 89 FHRVIKDF 96
|||||||

RESULT 9
CYP6_YEAST
ID CYP6_YEAST STANDARD; PRT; 371 AA.
AC P53691;

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CPR6 (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE).
GN CPR6 OR YLR216C OR L8167.24.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=97027304; PubMed=8873448;
RA Duina A.A., Marsh J.A., Gaber R.F.;
RT Identification of two Cyp-40-like cyclophilins in Saccharomyces
RT cerevisiae, one of which is required for normal growth.";
RL Yeast 12:943-952(1996).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favella A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Mardis E.,
RA Meneses S., Miller N., Nhan M., Pauley A., Peluso D., Rifkin L.,
RA Riles L., Taich S., Trevaskis E., Vaudin M., Vignati D.,
RA Wilcox L., Wilson R., Wohlman P., Waterston R.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBUNIT: INTERACTS WITH RPD3.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC CYP-40 SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U48867; AAC49414.1; -;
DR EMBL; U14913; AAB67445.1; -;
DR HSSP; P05092; IAWV.
DR SGD; S0004206; CPR6.
DR InterPro: IPR0021130; CSA_PPIase.
DR InterPro: IPR001440; TPR.
DR Pfam; PF00160; pro_isomerase; 1.
DR Pfam; PF00515; TPR; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; FALSE_NEG.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
DR Isomerase; Rotamase.
FT DOMAIN 1 175 PPIASE, CYCLOPHILIN-TYPE.
SQ SEQUENCE 371 AA; 42072 MW; 1886660D9486DDDD CRC64;

Query Match 89.8%; Score 44; DB 1; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FHRVIKDF 9
Db 62 FHRVIKDF 69
|||||||

RESULT 10
CYP5_CAEEL
ID CYP5_CAEEL STANDARD; PRT; 204 AA.
AC P52013;
DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
 DE (CYCLOPHILIN-5).
 GN CYP-5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=96276416; PubMed=8694762;
 RA Page A.P., Macniven K., Hengartner M.O.;
 RT "Cloning and biochemical characterization of the cyclophilin
 RL homologues from the free-living nematode Caenorhabditis elegans.";
 RL Biochem. J. 317:179-185(1996).
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U31948; AAC47126.1; -.
 DR HSSP; P23284; 1CYN.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase; Multigene family.
 SQ SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;

 Query Match 87.8%; Score 43; DB 1; Length 204;
 Best Local Similarity 88.9%; Pred. No. 0.21;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 KHRVVKDF 9
 ||||| ||
 DB 77 KHRVIADF 85

 RESULT 11
 CYP4_ARATH
 ID CYP4_ARATH STANDARD; PRT; 260 AA.
 AC P34791;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR
 DE (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING
 DE PROTEIN).
 GN ROC4 OR F21F14.200.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA; TISSUE=Leaf;
 RX MEDLINE=94179146; PubMed=8132503;
 RA Lippuner V., Chou I.T., Scott S.V., Ettinger W.F., Theng S.M.,
 RA Gasser C.S.;
 RT "Cloning and characterization of chloroplast and cytosolic forms of

cyclophilin from Arabidopsis thaliana.";
 J. Biol. Chem. 269:7863-7868(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=98088013; PubMed=9426607;
 RA Chou I.T., Gasser C.S.;
 RT "Characterization of the cyclophilin gene family of Arabidopsis
 RT thaliana and phylogenetic analysis of known cyclophilin proteins.";
 RL Plant Mol. Biol. 35:873-892(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Choine N., Robert C., Brottier P., Wincker P., Cattolico L.,
 RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.-W., Lemcke K.,
 RA Mayer K.F.X., Quetier F., Salanoubat M.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
 CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L14845; AAA20048.1; -.
 DR EMBL; U42724; AAB96831.1; -.
 DR EMBL; ALI38642; CAB71910.1; -.
 DR HSSP; P23284; 1CYN.
 DR SWISS-2DPAGE; P34791; ARATH.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Chloroplast; Transit peptide;
 KW Multigene family.
 FT TRANSIT 1 78 CHLOROPLAST (POTENTIAL).
 FT CHAIN 79 260 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
 SQ SEQUENCE 260 AA; 28208 MW; D412AECBB8A5A3B7 CRC64;

 Query Match 87.8%; Score 43; DB 1; Length 260;
 Best Local Similarity 87.5%; Pred. No. 0.28;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 2 FHRVVKDF 9
 ||||| ||
 DB 144 FHRVKDF 151

 RESULT 12
 CYPB_RAT
 ID CYPB_RAT STANDARD; PRT; 208 AA.
 AC P24368;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
 GN PP1B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN	SEQUENCE FROM N.A.
RP	MEDLINE-90300692; PubMed-2194066;
RX	Iwai N., Inagami T.;
RA	"Molecular cloning of a complementary DNA to rat cyclophilin-like
RT	protein mRNA.";
RL	kidney Int. 37:1460-1465(1990).
[2]	
RN	REVISIONS TO C-TERMINUS.
RP	MEDLINE-92112948; PubMed-1530944;
RX	Arber S., Krause K.H., Caroni P.;
RA	"S-cyclophilin is retained intracellularly via a unique COOH-terminal
RT	sequence and colocalizes with the calcium storage protein
RL	calreticulin.";
RT	J. Cell Biol. 116:113-125(1992).
CC	-1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC	-1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC	PEPTIDE BONDS IN OLIGOPEPTIDES.
CC	-1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC	-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
DR	HSP; P23284; ICLN.
DR	InterPro: IPR002130; CSA_PPIase.
DR	Pfam: PF00160; pro-isomerase; 1.
DR	PRINTS; PR00153; CSAPPISMRASE.
DR	PROSITE; PS00170; CSA_PPIASE_1; 1.
DR	PROSITE; PS50072; CSA_PPIASE_2; 1.
KW	Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW	Multigene family.
FT	SIGNAL 1 25 BY SIMILARITY.
FT	CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT	STATE 199 208 PREVENT SECRETION FROM ER
FT	(BY SIMILARITY).
FT	SEQUENCE 208 AA; 23025 MW; 76D12AC3427FEF32 CRC64;
SQ	

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Query Match      83.7%:  Score 41:  DB 1:  Length 208:  .
Best Local Similarity 77.8%: pred. No. 0.53:
Matches 7:  Conservative 1:  Mismatches 1:  Indels 0:  Gaps 0:
QY      1 KFRHVRVIKDF 9
      ||| : ||||
Db      84 KFRHMIKDF 92

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RESULT 13
CYP4_CAEEL
ID CYP4_CAEEL STANDARD; PRT; 523 AA..
AC P52012; Q09548;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 4 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE DE (CYCLOPHILIN-4).
OS CYP-4 OR F59E10.2.
GN Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Page A.P.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBDJ databases.
RN [2]
RP SEQUENCE OF 255-435 FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=96276416; PubMed=8694762;
RA Page A.P., Macniven K., Hengartner M.O.;
RT "Cloning and biochemical characterization of the cyclophilin
RT homologues from the free-living nematode Caenorhabditis elegans.";
RL Biochem. J. 317:179-185(1996).
RN [3]

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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Swinburne J., Palmer S.;
submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: PPIASE ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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EMBL; U36187; AAC06337.1; -.
EMBL; Z36949; CAA85417.1; -.
EMBL; Z46935; CAA85417.1; JOINED.
EMBL; Z46935; CAA87053.1; -.
EMBL; Z36949; CAA87053.1; JOINED.
EMBL; Z27450; IA58.
WormPep; F59E10.2; CE01596.
InterPro; IPR002130; CSA_PPIase.
InterPro; IPR003613; Ubox.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASMRASE..
SMART; SM00504; Ubox; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Isomerase; Rotamase; Isomerase family.
SEQUENCE 523 AA; 58533 MW; 399967AG6303989DE CRC64;

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Query Match      83.78; Score 41; DB 1; Length 523;
Best Local Similarity 77.8%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KFRHVIKDF 9
Db      320 KFHRLIKNF 328
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RESULT 14
CYP6_CABEL
ID CYP6_CABEL STANDARD; PRT; 201 AA.
AC P52014;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PRTIDYL-PROLYL CIS-TRANS ISOMERASE 6 PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN-6).
GN CYP-6 OR F42G9.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA MEDLINE=96276416; PubMed=8694762;
RX Page A.P., Macniven K., Hengartner M.O.;
RT "Cloning and biochemical characterization of the cyclophilin
RT homologues from the free-living nematode Caenorhabditis elegans.";
RL Biochem. J. 317:179-185(1996).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Taich A.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

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X-RAY CRYSTALLOGRAPHY (2.47 ANGSTROMS) OF 1-177.
MEDLINE=20108543; PubMed=10642184;
Ellis P.J., Carlow C.K.S., Ma D., Kuhn P.;
*Crystal structure of the complex of brugia malayi cyclophilin and
rt cyclosporin A.;
RL Biochemistry 39:592-598(2000).
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- ENZYME REGULATION: RELATIVELY INSENSITIVE TO INHIBITION BY CSA.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----
EMBL: L37292; AAC37249.1; -.
DR PDB: 1A58; 27-MAY-98.
DR PDB: 1A33; 29-JUL-98.
DR PDB: 1C5F; 02-DEC-99.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase; 3D-structure.
FT DOMAIN 10 175 PPIASE, CYCLOPHILIN-TYPE.
FT DOMAIN 700 709 POLY-ARG.
FT DOMAIN 713 716 POLY-ARG.
FT DOMAIN 800 815 POLY-SER.
FT DOMAIN 828 837 POLY-SER.
SQ SEQUENCE 843 AA; 97817 MW; 3C34EC90A32EDBDC CRC64;

Query Match 79.6%; Score 39; DB 1; Length 843;
Best Local Similarity 87.5%; Pred. No. 5.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIKDF 9
Db 64 FHRVIKDF 71

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Search completed: January 15, 2002, 13:14:58
Job time: 654 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:05:29 ; Search time 78.85 seconds
(without alignments)
16.696 Million cell updates/sec

Title: US-09-720-469-1
Perfect score: 49
Sequence: 1 KPHRVIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	203	Q01490	Q01490 orpinomyces
2	49	100.0	208	11 O88541	O88541 rattus norv
3	49	100.0	216	4 Q9BVK5	Q9BVK5 homo sapien
4	49	100.0	216	11 Q9PCY1	Q9PCY1 mus musculu
5	48	98.0	166	4 Q9Y3C6	Q9Y3C6 mus sapien
6	48	98.0	166	11 Q9D0W5	Q9D0W5 mus musculu
7	48	98.0	205	5 Q9W227	Q9W227 drosophila
8	45	91.8	104	13 Q98UE5	Q98UE5 xenopus lae
9	45	91.8	199	10 Q9ZVJ4	Q9ZVJ4 arabidopsis
10	44	89.8	145	10 Q9ATC5	Q9ATC5 vaucheria l
11	44	89.8	167	5 Q15729	Q15729 entamoeba h
12	44	89.8	173	10 Q9FW22	Q9FW22 oryza sativ
13	44	89.8	177	4 Q43447	Q43447 homo sapien
14	44	89.8	177	11 Q9CQU7	Q9CQU7 mus musculu
15	44	89.8	183	5 Q9V9B9	Q9V9B9 drosophila
16	44	89.8	188	11 Q9D868	Q9D868 mus musculu
17	44	89.8	189	10 Q9ZRQ9	Q9ZRQ9 pseudotsuga
18	44	89.8	210	5 Q9U6U5	Q9U6U5 plasmodium
19	44	89.8	210	5 Q27716	Q27716 plasmodium

20	44	89.8	214	3	Q94190	emericella
21	44	89.8	226	3	Q93826	trichophyto
22	43	87.8	73	11	O70134	mus musculu
23	43	87.8	144	5	Q9VAM2	drosophila
24	43	87.8	185	5	Q9GP41	echinococcu
25	43	87.8	196	2	Q9CH46	lactococcu
26	43	87.8	204	5	O62190	caenorhabdi
27	43	87.8	231	10	Q9AQU0	oryza sativ
28	43	87.8	260	10	Q9FPH5	arabidopsis
29	43	87.8	752	11	O55035	rattus norv
30	43	87.8	754	4	Q13427	homo sapien
31	43	87.8	970	5	Q9VAM1	drosophila
32	42	85.7	164	10	Q9STH1	arabidopsis
33	41	83.7	156	5	Q9N162	dictyosteli
34	41	83.7	259	10	Q9FY98	arabidopsis
35	41	83.7	259	10	O9ASS6	arabidopsis
36	41	83.7	356	3	Q11004	schizosacch
37	41	83.7	507	5	O76826	caenorhabdi
38	41	83.7	526	5	O76824	brugia mala
39	40	81.6	176	5	Q9W0Q2	drosophila
40	40	81.6	526	5	O76964	onchocerca
41	40	81.6	527	5	O61300	dirofilaria
42	39	79.6	174	5	Q9UA41	dictyosteli
43	39	79.6	197	2	Q99VD4	staphylococ
44	39	79.6	213	5	O96877	onchocerca
45	39	79.6	268	2	Q9A156	streptococc

ALIGNMENTS

RESULT	1
Q01490	
ID	Q01490
AC	Q01490
DT	01-NOV-1998 (TRENBLrel. 08, Created)
DT	01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT	01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE	(CYCLOPHILIN B) (ROTAMASE).
GN	CYPB.
OS	Orpinomyces sp. PC-2.
OC	Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
OC	Neocallimasticales; Orpinomyces.
OX	NCBI_TaxID=50059;
RN	[1]
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
RX	MEDLINE=95223986; PubMed=7708690;
RA	Chen H., Li X.-L., Ljungdahl L.G.;
RT	"A cyclophilin from the polycentric anaerobic rumen fungus Orpinomyces
RL	sp. strain PC-2 is highly homologous to vertebrate cyclophilin B.;"
CC	Proc. Natl. Acad. Sci. U.S.A. 92:2587-2591(1995).
CC	- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC	- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC	PEPTIDE BONDS IN OLIGOPEPTIDES.
CC	- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC	- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC	- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
DR	EMBL; U17900; AAD04195.1; -
DR	HSSP; P23284; 1CYN.
DR	Mendel; 20786; Unkp;1040;20786.
DR	InterPro; IPR002130; CSA_PPIase.
DR	Pfam; PF00160; pro_isomerase.1.
DR	PRINTS; PR00153; CSAPPISMRASE.
DR	PROSITE; PS00170; CSA_PPIASE_1; 1.
DR	PROSITE; PS00072; CSA_PPIASE_2; 1.
DR	Isomerase; Rotamase; Signal; Cyclosporin; Endoplasmic reticulum.
FT	SIGNAL 1 22
FT	CHAIN 23 203 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT	BINDING 147 147 CSA (POTENTIAL).
FT	SITE 200 203 PREVENT SECRETION FROM ER (BY
FT	SIMILARITY).
SO	SEQUENCE 203 AA; 21969 MW; A5748C94305B8BE0 CRC64;

Query Match 100.0%; Score 49; DB 3; Length 203;

Best Local Similarity 100.0%; Pred. No. 0.066; 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHVRVKDF 9
| | | | | | | | |

Db 78 KFHVRVKDF 86

RESULT 2

ID O88541 PRELIMINARY; PRT; 208 AA.

AC O88541; 1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE CYCLOPHILIN B (EC 5.2.1.8).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

FN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WISTAR-KYOTO; TISSUE=KIDNEY;

RA Kainer D.B., Doris P.A.;

RT "Cyclophilin B";

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE

FOLDING OF PROTEINS (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-

TRANS ISOMERASE FAMILY.

DR EMBL; AF071225; AAC25590.1; -.

DR HSSP; P23284; ICYN.

DR InterPro; IPR002130; CSA_PPIase.

DR Pfam; PF00160; pro_isomerase; 1.

DR PRINTS; PR00153; CSAPPISMRASE.

DR PROSITE; PS00170; CSA_PPIase_1; 1.

DR PROSITE; PS00072; CSA_PPIase_2; 1.

Qy Isomerase; Rotanase.

SW SEQUENCE 208 AA; 22802 MW; 02408DFA7157218C CRC64;

Query Match 100.0%; Score 49; DB 11; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.068; 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHVRVKDF 9
| | | | | | | | |

Db 84 KFHVRVKDF 92

RESULT 3

ID Q9BVK5 PRELIMINARY; PRT; 216 AA.

AC Q9BVK5;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

FN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SKIN, AND MELANOMA;

RA Strausberg R.;

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC001125; AAH01125.1; -.

KW Isomerase.
SQ SEQUENCE 216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;

Query Match 100.0%; Score 49; DB 4; Length 216;

Best Local Similarity 100.0%; Pred. No. 0.071; 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHVRVKDF 9
| | | | | | | | |

Db 92 KFHVRVKDF 100

RESULT 4

ID Q9DCY1 PRELIMINARY; PRT; 216 AA.

AC Q9DCY1;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE PEPTIDYLPROLYL ISOMERASE B.

GN PPIB.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

FN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=KIDNEY;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Flieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Grinstein S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauer P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).

DR EMBL; AK002357; BAB22036.1; -.

DR MGD; MGI:97750; Ppib.

DR InterPro; IPR002130; CSA_PPIase.

DR Pfam; PF00160; pro_isomerase; 1.

DR PRINTS; PR00153; CSAPPISMRASE.

DR PROSITE; PS00072; CSA_PPIase_2; 1.

Qy SEQUENCE 216 AA; 23713 MW; CE9DAD1544AE72FE CRC64;

Query Match 100.0%; Score 49; DB 11; Length 216;

Best Local Similarity 100.0%; Pred. No. 0.071; 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHVRVKDF 9
| | | | | | | | |

Db 92 KFHVRVKDF 100

RESULT 5

ID Q9V3C6 PRELIMINARY; PRT; 166 AA.

AC Q9V3C6;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 CGT-124 PROTEIN (EC 5.2.1.8).
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RA Lip W.-C.;
 RT "Comparative gene cloning: Identification of novel human genes with
 Caenorhabditis elegans proteome as template.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RA TISSUE-LYMPHOMA;
 RC Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 TRANS ISOMERASE FAMILY.
 DR EMBL; AF151882; AAD34119.1; -;
 DR HSSP; P05092; 2RMC.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPLSMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS50072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 166 AA; 18237 MW; 2872DC3336CD05E4 CRC64;

Query Match 98.0%; Score 48; DB 4; Length 166;
 Best Local Similarity 88.9%; Pred. No. 0.084;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFHRIKDF 9
 |||||
 DB 52 KFHRIKDF 60

RESULT 6
 ID Q9D0W5 PRELIMINARY; PRT; 166 AA.
 AC Q9D0W5
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DE 1110060010R1K PROTEIN.
 GN 1110060010R1K
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 TRANS ISOMERASE FAMILY.
 DR EMBL; AK004331; BAB23265.1; -;
 DR MGD; MGI:1916066; 1110060010R1K.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPLSMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS50072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 166 AA; 18237 MW; A5C5B04FE29C52C9 CRC64;

Query Match 98.0%; Score 48; DB 11; Length 166;
 Best Local Similarity 88.9%; Pred. No. 0.084;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFHRIKDF 9
 |||||
 DB 52 KFHRIKDF 60

RESULT 7
 ID Q9W227 PRELIMINARY; PRT; 205 AA.
 AC Q9W227
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CG2852 PROTEIN.
 GN CG2852
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20195006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.F., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandell W.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwey L.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merklov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 CC FOLDING OF PROTEINS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 CC TRANS ISOMERASE FAMILY.
 CC EMBL: AE003458; AAF46873.1; -.
 DR HSP; P23284; ICYN
 DR FlyBase; FBgn0034753; CG2852.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS50072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 205 AA; 22199 MW; A9CEFB8B1CC813F7 CRC64;

Query Match 98.0%; Score 48; DB 5; Length 205;
 Best Local Similarity 88.9%; Pred. No. 0.11;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHRIKDF 9
 Db 77 KFHRIKDF 85
 |||||

RESULT 8
 Q98UE5 PRELIMINARY; PRT; 104 AA.
 ID Q98UE5
 AC Q98UE5
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 CC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8355;
 OX [1]
 RN SEQUENCE FROM N.A.
 RA Amano T., Yoshizato K.;
 RA "Isolation of genes involved in intestinal remodeling during anuran
 RT metamorphosis.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF170328; AAK11503.1; -.
 KW Isomerase.
 FT NON_TER 104 104
 SQ SEQUENCE 104 AA; 11350 MW; 8F6AD1C1C2FB3E2 CRC64;

Query Match 91.8%; Score 45; DB 13; Length 104;
 Best Local Similarity 88.9%; Pred. No. 0.2;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHRIKDF 9
 Db 84 KFHRIKDF 92
 |||||

RESULT 9
 Q92VJ4 PRELIMINARY; PRT; 199 AA.
 ID Q92VJ4
 AC Q92VJ4
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE PUTATIVE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
 GN T6A23.7
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 CC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
 RA Shen M., Renning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
 RT "Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC005499; AAC67345.1; -.
 DR HSP; P05092; 2CPL.
 DR Mendel; 38509; Arath; 1040; 38509.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS50072; CSA_PPIASE_2; 1.
 KW Isomerase.
 SQ SEQUENCE 199 AA; 21492 MW; FCC6DAH546C68C8C CRC64;

Query Match 91.8%; Score 45; DB 10; Length 199;
 Best Local Similarity 88.9%; Pred. No. 0.39;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHRIKDF 9
 Db 85 QFHRIKDF 93
 |||||

RESULT 10
 Q9ATC5 PRELIMINARY; PRT; 145 AA.
 ID Q9ATC5
 AC Q9ATC5
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CYCLOPHILIN (FRAGMENT).
 OS Vaucheria litorea.
 CC Eukaryota; stramenopiles; Xanthophyceae; Vaucheriales; Vaucheriaceae;
 CC Vaucheria.
 CC NCBI_TaxID=109269;
 OX [1]
 RN SEQUENCE FROM N.A.
 RA Summer E.J., Rumpho M.E.;
 RA "Chloroplast localized, nuclear encoded proteins persist for many
 RT months in an animal cell despite the lack of cognate algal nuclear
 RT genes.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF336984; AAK21908.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 145 AA; 15303 MW; CFCBA0B72D42EA09 CRC64;

Query Match 89.8%; Score 44; DB 10; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.44;

```
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIKDF 9
DB 33 FHRVIKDF 40

RESULT 11
OI15729 PRELIMINARY; PRT; 167 AA.
AC OI15729
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYCLOPHILIN (EC 5.2.1.8).
GN Cyp1.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RC STRAIN=HM1:IMSS;
RA Carrero J.C.; Petrossian P.; Acosta-Camarena E.; Ostoa-Saloma P.;
RA Ortiz-Ortiz L.; Laclette J.P.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RA Carrero J.C.; Petrossian P.; Acosta-Camarena E.; Ostoa-Saloma P.;
RA Ortiz-Ortiz L.; Laclette J.P.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; AF017993; AAB86601.1; -.
DR HSSP; P05092; 2CPL.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase.1.
DR PRINTS; PR00153; CSA_PPIase.1.
DR PROSITE; PS00170; CSA_PPIase_1; 1.
DR PROSITE; PS50072; CSA_PPIase_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 167 AA; 18139 MW; DBA23F5BB3290B2 CRC64;

Query Match 89.8%; Score 44; DB 5; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIKDF 9
DB 55 FHRVIKDF 62

RESULT 12
Q9FW22 PRELIMINARY; PRT; 173 AA.
ID Q9FW22
AC Q9FW22
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SIMILAR TO ARABIDOPSIS THALIANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
DE (P34791) (FRAGMENT).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RC SEQUENCE FROM N.A.
```

```
RA Hsing Y.-I.C.; Chow T.-Y.; Wu H.-P.; Chao Y.-T.; Liu S.-M.;
RA Chen C.-S.; Shaw J.-F.;
RL "Oryza sativa PAC P0036D10 genomics sequence, complete sequence.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC073405; AAG03106.1; -.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase.1.
DR PRINTS; PR00153; CSA_PPIase.1.
DR PROSITE; PS50072; CSA_PPIase_2; 1.
DR NON_TER 173 173
SQ SEQUENCE 173 AA; 19158 MW; 28EAD80F4625EB9 CRC64;

Query Match 89.8%; Score 44; DB 10; Length 173;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIKDF 9
DB 86 FHRVIKDF 93

RESULT 13
OI43447 PRELIMINARY; PRT; 177 AA.
ID OI43447
AC OI43447
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE U-SNRNP-ASSOCIATED CYCLOPHILIN (EC 5.2.1.8).
GN USA-CVP OR CVP-20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RA Teigelkamp S.; Achsel T.; Mundt C.; Gothel S.F.; Cronshagen U.;
RX MEDLINE-98067393; PubMed-9404889;
RA Horowitz D.S.; Kobayashi R.; Krainer A.R.;
RT "A new cyclophilin and the human homologues of yeast Prp3 and Prp4
RT form a complex associated with U4/U6 snRNPs.";
RL RNA 3:1374-1387(1997).
RN [2]
RC SEQUENCE FROM N.A.
RA Teigelkamp S.; Achsel T.; Mundt C.; Gothel S.F.; Cronshagen U.;
RX MEDLINE-98230239; PubMed-9570313;
RA Lane W.S.; Marahiel M.; Luhrmann R.;
RT "The 20kD protein of human [U4/U6.U5] tri-snRNPs is a novel
RT cyclophilin that forms a complex with the U4/U6-specific 60kD and 90kD
RT proteins.";
RL RNA 4:127-141(1998).
RN [3]
RC SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; AF016371; AAC51927.1; -.
DR EMBL; AF036331; AAC60793.1; -.
DR EMBL; BC003412; AAH03412.1; -.
DR HSSP; P05092; 2RMC.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase.1.
DR PRINTS; PR00153; CSA_PPIase.1.
DR PROSITE; PS00170; CSA_PPIase_1; 1.
DR PROSITE; PS50072; CSA_PPIase_2; 1.
KW Isomerase; Rotamase.
```

SQ SEQUENCE 177 AA; 19208 MW; 566BCE6361E0F339 CRC64;

Query Match 89.8%; Score 44; DB 4; Length 177;

Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVVKDF 9

Db 65 FHRVVKDF 72

RESULT 14

Q9CQU7 Q9CQU7 PRELIMINARY; PRT; 177 AA.

AC Q9CQU7 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE 4833408F11RIK OR 1100001J08RIK PROTEIN.

GN 4833408F11RIK OR 1100001J08RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=HEAD, EMBRYO, AND CEREBELLUM;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,

RA Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE

CC FOLDING OF PROTEINS (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

CC PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-

CC TRANS ISOMERASE FAMILY.

CC EMBL: AK014665; BAB29493.1; -

DR EMBL: AK003179; BAB22623.1; -

DR EMBL: AK005202; BAB23880.1; -

DR MGD: MGI:1913351; 1100001J08RIK.

DR MGD: MGI:1921150; 4833408F11RIK.

DR InterPro: IPR002130; CSA_PPIase.

DR Pfam: PF00160; pro_isomerase.1.

DR PRINTS: PR00153; CSAPPISMRASE.

DR PROSITE: PS00170; CSA_PPIASE_1; 1.

DR PROSITE: PS00072; CSA_PPIASE_2; 1.

KW Isomerase; Rotamase.

SQ SEQUENCE 177 AA; 19208 MW; 566BCE6361E0F339 CRC64;

Query Match

Best Local Similarity 89.8%; Score 44; DB 11; Length 177;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVVKDF 9

Db 65 FHRVVKDF 72

RESULT 15

Q9V9B9 Q9V9B9 PRELIMINARY; PRT; 183 AA.

AC Q9V9B9 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE CG17266 PROTEIN.

GN CG17266.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fosler G., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hartis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

DR EMBL: AE003789; AAF57375.1; -

DR HSP: P05092; 2CPL.

DR FlyBase: FBgn0033089; CG17266.

DR InterPro: IPR002130; CSA_PPIase.

DR Pfam: PF00160; pro_isomerase.1.

DR PRINTS: PR00153; CSAPPISMRASE.

DR PROSITE: PS00072; CSA_PPIASE_2; 1.

SQ SEQUENCE 183 AA; 20182 MW; 19E5CE187CH9E949 CRC64;

Query Match

Best Local Similarity 89.8%; Score 44; DB 5; Length 183;

Matches 8; Conservative 100.0%; Pred. No. 0.56;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 FHRVIKDF 9
 |||||||
DB 71 FHRVIKDF 78

Search completed: January 15, 2002, 13:16:24
Job time: 655 sec

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:02:09 ; Search time 81.32 Seconds
(Without alignments)
8.198 Million cell updates/sec

Title: US-09-720-469-1
Sequence: 1 KHRVTKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	49	100.0	9	21	AAV69921 Human cyclophilin
2	49	100.0	9	22	AA846930 Human cyclophilin
3	49	100.0	166	21	AAG00090 Human secreted pro
4	49	100.0	211	22	AA873302 Human cyclophilin
5	49	100.0	216	22	AA873301 Human cyclophilin
6	49	100.0	291	21	AA843878 Human cancer assoc
7	48	98.0	113	21	AAG03983 Human secreted pro
8	48	98.0	166	22	AAU12175 Human PRO4984 poly
9	48	98.0	178	22	AA875471 Human colon cancer
10	46	93.9	9	21	AAV69962 Human cyclophilin
11	46	93.9	9	22	AA846946 Human cyclophilin

12	44	89.8	183	21	AA856701 Human prostate can
13	44	89.8	212	14	AA832353 Cyclophilin C. Mu
14	44	89.8	212	21	AAV92048 A. niger peptidyl-
15	43	87.8	252	21	AA816463 Arabidopsis thalia
16	43	87.8	254	21	AA816462 Arabidopsis thalia
17	43	87.8	260	21	AA816461 Arabidopsis thalia
18	43	87.8	987	22	AA846633 Amino acid sequenc
19	42	85.7	105	21	AA837614 Arabidopsis thalia
20	42	85.7	112	21	AA837613 Arabidopsis thalia
21	42	85.7	129	21	AA837612 Arabidopsis thalia
22	42	85.7	140	21	AA811445 Arabidopsis thalia
23	42	85.7	140	21	AA832372 Arabidopsis thalia
24	42	85.7	147	21	AA811444 Arabidopsis thalia
25	42	85.7	147	21	AA832371 Arabidopsis thalia
26	42	85.7	164	21	AA811443 Arabidopsis thalia
27	42	85.7	164	21	AA832370 Arabidopsis thalia
28	41	83.7	254	21	AA805073 Arabidopsis thalia
29	41	83.7	259	21	AA805072 Arabidopsis thalia
30	41	83.7	523	22	AA849138 Arabidopsis thalia
31	40	81.6	527	22	AA849136 D.immitis cyclophi
32	40	81.6	527	22	AA849137 D.immitis tyrosine
33	39	79.6	269	22	AA849140 Human nuclear-spec
34	39	79.6	589	16	AA874292 B. malayi cyclosp
35	38	77.6	162	12	AA810784 yeast peptidyl-pro
36	38	77.6	162	16	AA872962 yeast peptidyl pro
37	38	77.6	162	16	AA872918 yeast peptidyl pro
38	38	77.6	163	21	AA830405 Arabidopsis thalia
39	38	77.6	163	21	AA850215 Arabidopsis thalia
40	38	77.6	171	22	AA849141 Caenorhabditis ele
41	38	77.6	172	21	AA830404 Arabidopsis thalia
42	38	77.6	172	21	AA850214 Arabidopsis thalia
43	38	77.6	192	21	AA850213 Arabidopsis thalia
44	38	77.6	193	21	AA830403 Arabidopsis thalia
45	38	77.6	982	12	AA813320 Murine Natural Kil

ALIGNMENTS

RESULT 1
AAV69921
ID AAV69921 standard; peptide; 9 AA.
AC AAV69921;
XX
XX 11-APR-2000 (first entry)
DT
XX Human cyclophilin B peptide fragment #1.
DE
XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
XX WO9967288-A1.
PN
XX 29-DEC-1999.
PD
XX 24-JUN-1999; 99WO-JP03360.
PF
XX 25-JUN-1998; 98JP-0178449.
PR
XX (SUMU) SUMITOMO PHARM CO LTD.
XX (ITOHI) ITOH K.
PA
XX Itoh K, Gomi S;
XX WPI; 2000-116932/10.
DR
XX Tumour antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumours
XX
XX Claim 4; Page 49; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHVRVKDF 9
 | | | | | | | |
 Db 1 kfhrvikdf 9

RESULT 2
 AAB46930
 ID AAB46930 standard; peptide; 9 AA.
 AC AAB46930;
 XX
 XX
 DT 04-MAY-2001 (first entry)
 XX Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.
 DE
 XX Tumor antigenic peptide; Interferon; IFN; antigen-specific T cell;
 KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
 KW viral infectious disease; cyclophilin B; human.
 XX
 XX Homo sapiens.
 OS
 XX EP1074267-A1.
 PN
 PD 07-FEB-2001.
 XX
 PF 24-JUL-2000; 2000EP-0306263.
 XX
 XX 22-JUL-1999; 99JP-0207687.
 PR
 XX (SUMU) SUMITOMO PHARM CO LTD.
 PA
 XX Takasu H, Gotoh M, Yamaoka T;
 PI
 PT WPI; 2001-193144/20.
 DR
 XX Use of antigenic proteins, peptides, interferon or their encoding DNA,
 PT in the manufacture of an agent for the induction of antigen-specific T
 PT cells -
 XX
 XX Disclosure; Page 15; 25pp; English.
 PS
 XX This invention describes the novel use of interferons (IFNs) or DNAs
 CC capable of expressing the interferons and/or antigenic proteins (AP),
 CC antigenic peptides derived from the proteins or DNAs capable of
 CC expressing the antigenic proteins or peptides, in the manufacture of
 CC an agent for induction of antigen-specific T cells. The products of
 CC the invention have virucide and cytostatic activity and can be used for
 CC gene therapy or as inducers of antigen-specific T cells. The action of
 CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
 CC T cell (CTL) by administering an antigenic peptide in an incomplete
 CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
 CC DNA encoding IFNs) are useful in the manufacture of a medicament for
 CC inducing antigen-specific T cells in an individual who has been
 CC administered with AP (or DNA encoding AP) or vice versa. The medicament
 CC is useful for the treatment or prophylaxis of a tumor or a viral
 CC infectious disease.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHVRVKDF 9
 | | | | | | | |
 Db 1 kfhrvikdf 9

RESULT 3
 AAG00090
 ID AAG00090 standard; Protein; 166 AA.
 XX AAG00090;
 AC
 XX
 DT 06-OCT-2000 (first entry)
 XX Human secreted protein, SEQ ID NO: 4171.
 DE
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 KW
 XX Homo sapiens.
 OS
 XX EP1033401-A2.
 PN
 XX 06-SEP-2000.
 PD
 XX 21-FEB-2000; 2000EP-0200610.
 PF
 XX 26-FEB-1999; 99US-0122487.
 PR
 XX (GEST) GENSET.
 XX
 PA Dumas Milne Edwards J, Duclert A, Giordano J;
 PI
 XX WPI; 2000-500381/45.
 DR
 XX N-PSDB; AAC00096.
 DR
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 PT
 XX Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
 PS
 XX The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full-length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.
 XX
 SQ Sequence 166 AA;

Query Match 100.0%; Score 49; DB 21; Length 166;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFHVRVKDF 9
 | | | | | | | |
 Db 92 kfhrvikdf 100

RESULT 4
 AAB73302

ID XX AAB73302 standard; protein; 211 AA.
 AC XX AAB73302;
 XX DT 22-MAY-2001 (first entry)
 XX DE Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
 XX KW Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
 KW somatolactogenic function modulator; immunosuppression; short stature;
 KW muscle wasting; osteoporosis; HIV infection; breast cancer;
 KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia;
 KW C-terminal deletion mutant; mutein.
 XX OS Homo sapiens.
 XX PN WO200113113-A1.
 XX PD 22-FEB-2001.
 XX PF 10-AUG-2000; 2000WO-US21789.
 XX PR 19-AUG-1999; 99US-0149752.
 XX PA (UYPE-) UNIV PENNSYLVANIA.
 XX PI Clevenger CV, Ryczyn MA;
 XX DR WPI; 2001-211249/21.
 XX PT Novel composition for modulating somatolactogenic function, comprises
 PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
 PT B with somatolactogenic hormone
 PS Disclosure; Page -: 21pp; English.
 XX CC The invention relates to a composition for modulating somatolactogenic
 CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B
 CC (particularly a CypB mutant in which residues 2-12 of the mature protein
 CC are absent) or an inhibitor of the interaction of cyclophilin B with a
 CC somatolactogenic hormone (e.g., prolactin, growth hormone). The invention
 CC also relates to a method of identifying inhibitors of somatolactogenic
 CC functions using CypB and a somatolactogenic hormone, and a method for
 CC diagnosing diseases associated with abnormal somatolactogenic functions
 CC by assessing CypB levels in a sample from a patient. Cyclophilin B is
 CC useful for augmenting somatolactogenic function in the animal, and
 CC cyclophilin B mutant or a composition comprising an inhibitor of the
 CC interaction of cyclophilin B with a somatolactogenic hormone, is useful
 CC for inhibiting somatolactogenic function in the animal. A composition
 CC in the treatment of short stature, muscle wasting and osteoporosis. A
 CC composition comprising cyclophilin B mutant or a composition comprising
 CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic
 CC hormone, is useful for treating HIV infection, breast and prostate
 CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
 CC Note: The present sequence is not shown in the specification, but
 CC is derived from the wild-type CypB sequence shown on pages 17-18.
 XX SQ Sequence 211 AA;
 Query Match 100.0%; Score 49; DB 22; Length 211;
 Best Local Similarity 100.0%; Pred. No. 0.039;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFHRIKDF 9
 Db |||||
 92 kfhrikdff 100
 RESULT 5
 AAB73301
 ID XX AAB73301 standard; protein; 216 AA.
 AC XX AAB73301;
 XX DT 22-MAY-2001 (first entry)
 XX DE Human cyclophilin B (CypB).
 XX KW Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
 KW somatolactogenic function modulator; immunosuppression; short stature;
 KW muscle wasting; osteoporosis; HIV infection; breast cancer;
 KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
 XX OS Homo sapiens.
 XX PN WO200113113-A1.
 XX PD 22-FEB-2001.
 XX PF 10-AUG-2000; 2000WO-US21789.
 XX PR 19-AUG-1999; 99US-0149752.
 XX PA (UYPE-) UNIV PENNSYLVANIA.
 XX PI Clevenger CV, Ryczyn MA;
 XX DR WPI; 2001-211249/21.
 XX PT Novel composition for modulating somatolactogenic function, comprises
 PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
 PT B with somatolactogenic hormone
 PS Claim 1; Page 17-18; 21pp; English.
 XX CC The invention relates to a composition for modulating somatolactogenic
 CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B
 CC (particularly a CypB mutant in which residues 2-12 of the mature protein
 CC are absent) or an inhibitor of the interaction of cyclophilin B with a
 CC somatolactogenic hormone (e.g., prolactin, growth hormone). The invention
 CC also relates to a method of identifying inhibitors of somatolactogenic
 CC functions using CypB and a somatolactogenic hormone, and a method for
 CC diagnosing diseases associated with abnormal somatolactogenic functions
 CC by assessing CypB levels in a sample from a patient. Cyclophilin B is
 CC useful for augmenting somatolactogenic function in the animal, and
 CC cyclophilin B mutant or a composition comprising an inhibitor of the
 CC interaction of cyclophilin B with a somatolactogenic hormone, is useful
 CC for inhibiting somatolactogenic function in the animal. A composition
 CC in the treatment of short stature, muscle wasting and osteoporosis. A
 CC composition comprising cyclophilin B mutant or a composition comprising
 CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic
 CC hormone, is useful for treating HIV infection, breast and prostate
 CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
 CC sequence represents human cyclophilin B.
 XX SQ Sequence 216 AA;
 Query Match 100.0%; Score 49; DB 22; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFHRIKDF 9
 Db |||||
 92 kfhrikdff 100
 RESULT 6
 AAB43878
 ID XX AAB43878 standard; protein; 291 AA.
 AC XX AAB43878;
 Query Match 100.0%; Score 49; DB 22; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFHRIKDF 9
 Db |||||
 92 kfhrikdff 100
 RESULT 6
 AAB43878
 ID XX AAB43878 standard; protein; 291 AA.
 AC XX AAB43878;

```

XX 08-FEB-2001 (first entry)
XX Human cancer associated protein sequence SEQ ID NO:1323.
DE
XX Human; cancer associated gene; cancer antigen; detection; cancer;
XX diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
XX antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
XX dermatological; neuroprotective; thrombolytic; coagulant; neutropenic;
XX vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;
XX immune disorder; haematopoietic cell disorder; autoimmune disorder;
XX allergic reaction; graft versus host disease; organ rejection;
XX haemostatic; thrombolytic; cardiovascular disorder; infection;
XX neurological disease; drug screening.
XX
XX Homo sapiens.
OS
XX WO200055350-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05882.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
PI
XX WPI; 2000-587533/55.
XX
XX N-PSDB; AAC78087.
XX
XX Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer -
XX
XX Claim 11; Page 1974-1975; 2352pp; English.
XX
XX AAC77607 to AAC78448 encode the human cancer associated proteins given
XX in AAB43398 to AAB44239. The proteins can have activities based on the
XX tissues and cells the genes are expressed in. Example of activities
XX include: cytostatic; proliferative; vulnerary; immunomodulator;
XX antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
XX antiinflammatory; antithyroid; antiallergic; antibacterial;
XX dermatologic; neuroprotective; cardiant; thrombolytic; coagulant;
XX neutropic; vasotropic; antipsoriatic and antiangiogenic. The
XX polynucleotides and polypeptides can be used for preventing, treating or
XX ameliorating medical conditions and diagnosing pathological conditions.
XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from
XX the present invention may be used to treat immune disorders by activating
XX or inhibiting the proliferation, differentiation or mobilisation of
XX immune cells, to treat disorders of haematopoietic cells, autoimmune
XX disorders, allergic reactions, graft versus host disease and organ
XX rejection, modulate haemostatic or thrombolytic activity, modulate
XX inflammation, cancers, cardiovascular disorders, neurological disease and
XX bacterial or viral infections. The peptides, nucleotides, antibodies,
XX agonists and antagonists may be also be used in drug screens. AAC78449 to
XX AAC78457 and AAB44240 represent sequences used in the exemplification of
XX the present invention.
XX
XX Sequence 291 AA;
XX
XX Query Match 100.0%; Score 49; DB 21; Length 291;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 KFHVRVVKDF 9
XX |||||
XX 167 kfhrvikdf 175
XX
XX RESULT 7

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AAG03983
XX ID AAG03983 standard; Protein: 113 AA.
XX
XX AC AAG03983;
XX
XX DT 06-OCT-2000 (first entry)
XX
XX DE Human secreted protein, SEQ ID NO: 8064.
XX
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping..
XX
XX OS Homo sapiens.
XX
XX PN EP1033401-A2.
XX
XX PD 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX N-PSDB; AAC03989.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 13; SEQ ID 8064; 7lpp + CD-ROM; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number
XX of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
XX were prepared from total human RNAs or polyA+ RNAs derived from 30
XX different tissues. EST sequences usually correspond mainly to the 3'
XX untranslated region (UTR) of the mRNA because they are often obtained
XX from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
XX isolating cDNA sequences derived from the 5' ends of mRNAs and even in
XX those cases where longer cDNA sequences have been obtained, the full 5'
XX UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
XX ends and can therefore be used to obtain full length cDNAs and genomic
XX DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
XX chromosome mapping procedures. They are used to obtain upstream
XX regulatory sequences and to design expression and secretion vectors.
XX
XX SQ Sequence 113 AA;
XX
XX Query Match 98.0%; Score 48; DB 21; Length 113;
XX Best Local Similarity 88.9%; Pred. No. 0.032;
XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 KFHVRVVKDF 9
XX |||||
XX 52 kfhrvikdf 60
XX
XX RESULT 8
XX AAU12175
XX ID AAU12175 standard; Protein: 166 AA.
XX
XX XX AAU12175;
XX
XX AC AAU12175;
XX
XX DT 24-OCT-2001 (first entry)
XX
XX DE Human PRO4984 polypeptide sequence.
XX
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
XX breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;

```

KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
XX adipocyte; A-peptide; factor VIIA; gene therapy.
OS Homo sapiens.
XX WO200140466-A2.

PN 07-JUN-2001.

PD 01-DEC-2000; 2000WO-US32678.

PF 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.
XX 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99WO-US28565.
XX 09-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30092.
XX 16-DEC-1999; 99WO-US30092.

PR 20-DEC-1999; 99WO-US30911.
XX 20-DEC-1999; 99WO-US30911.

PR 30-DEC-1999; 99WO-US31243.
XX 30-DEC-1999; 99WO-US31243.

PR 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00277.

PR 11-FEB-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US00376.

PR 18-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04341.

PR 22-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04342.

PR 24-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US04914.

PR 01-MAR-2000; 2000WO-US05004.
XX 01-MAR-2000; 2000WO-US05004.

PR 21-MAR-2000; 2000WO-US05601.
XX 21-MAR-2000; 2000WO-US05601.

PR 21-MAR-2000; 2000WO-US07377.
XX 21-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 2000WO-US07532.
XX 30-MAR-2000; 2000WO-US07532.

PR 17-MAY-2000; 2000WO-US08439.
XX 17-MAY-2000; 2000WO-US08439.

PR 22-MAY-2000; 2000WO-US13705.
XX 22-MAY-2000; 2000WO-US13705.

PR 30-MAY-2000; 2000WO-US14042.
XX 30-MAY-2000; 2000WO-US14042.

PR 02-JUN-2000; 2000WO-US14941.
XX 02-JUN-2000; 2000WO-US14941.

PR 10-NOV-2000; 2000WO-US15264.
XX 10-NOV-2000; 2000WO-US15264.

XX (GETH) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-408281/43.
XX N-PSDB; AAS21247.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect
XX other PRO polypeptides, link bioactive molecules to cells expressing
XX PRO polypeptides, and detect the presence of mammalian tumours e.g.
XX lung, breast, prostate, cervical

XX Claim 12; Fig 8; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane
XX PRO polypeptides. The PRO polypeptides are useful to detect other
XX PRO polypeptides, to link bioactive molecules to cells expressing
XX PRO polypeptides, to modulate biological activities of cells expressing
XX PRO polypeptides, and to detect the presence of mammalian lung, colon,
XX breast, prostate, rectal, cervical or liver tumours by comparing PRO
XX polypeptide expression in a cell sample to that in a control sample.

XX Some of the 275 sequences are also useful to stimulate the release of
XX tumour necrosis factor-alpha (TNF-alpha) from human blood, the
XX proliferation or differentiation of chondrocytes, the proliferation or
XX gene expression in pericyte cells, the release of proteoglycans from
XX cartilage, the proliferation of inner ear utricular supporting cells or
XX of T-lymphocytes, the release of a cytokine from peripheral blood
XX monocytes (PBMCs), or the proliferation of endothelial cells. Some of
XX the PRO polypeptides may modulate glucose or free fatty acid uptake by
XX skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
XX to factor VIIA. The PRO polypeptides can be used in assays to identify
XX molecules involved in binding interactions. The polynucleotides encoding

CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX

SQ Sequence 166 AA;

Query Match 98.0%; Score 48; DB 22; Length 166;

Best Local Similarity 88.9%; Pred. No. 0.048;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KFRHVIKDF 9

Db 52 kfhrlikdf 60

||||:||||

RESULT 9

AAG75471

ID AAG75471 standard; Protein: 178 AA.

XX AC AAG75471;

XX DT 03-SEP-2001 (first entry)

XX DE Human colon cancer antigen protein SEQ ID NO:6235.

XX KW Human: colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma.

XX OS Homo sapiens.

XX PN WO200122920-A2.

XX PD 05-APR-2001.

XX PF 28-SEP-2000; 2000WO-US26524.

XX PR 29-SEP-1999; 99US-0157137.

XX PR 03-NOV-1999; 99US-0163280.

XX PR (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;

XX WPI; 2001-235357/24.

XX DR N-PSDB; AAH34876.

XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX Claim 11; Page 7683-7684; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of P by expressing
XX inactive proteins or to supplement the patients own production of P.
XX Additionally, N may be used to produce the colon cancer-associated Ps,
XX by inserting the nucleic acids into a host cell and culturing the cell
XX to express the proteins. N and P can be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
XX and AAB77789 represent sequences used in the exemplification of the
XX present invention.

XX N.B. Pages 666 to 682 and page 7053 of the sequence listing were
XX missing at time of publication, meaning no sequences are present for
XX SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 178 AA;

Query Match 98.0%; Score 48; DB 22; Length 178;
 Best Local Similarity 88.9%; Pred. No. 0.052;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KFHVRVVKDF 9
 |::|::|::|::|
 Db 64 kfhvrivkdf 72

RESULT 10

AAY69962
 ID AAY69962 standard; peptide; 9 AA.

XX AC AAY69962;

XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #42.

XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.

XX OS Homo sapiens.

XX PN WO9967288-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP03360.

XX PR 25-JUN-1998; 98JP-0178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PI (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;

XX WPI: 2000-116932/10.

XX PT Tumour antigen peptides derived from cyclophilin B for treatment and
 diagnosis of tumours

XX PS Claim 10; Page 60; 64pp; Japanese.

XX CC This sequence represents a cyclophilin B peptide of the invention. The
 peptides are tumour antigen peptides derived from cyclophilin B, that
 recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 peptides are used for the treatment and diagnosis of tumours.

XX SQ Sequence 9 AA;

Query Match 93.9%; Score 46; DB 21; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.3e+05;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KFHVRVVKDF 9
 |::|::|::|::|
 Db 1 kyhrvikdf 9

RESULT 11

AAB46946
 ID AAB46946 standard; peptide; 9 AA.

XX AC AAB46946;

XX DT 04-MAY-2001 (first entry)

XX DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 32.

XX KW Tumor antigenic peptide; Interferon; IFN; antigen-specific T cell;

KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
 viral infectious disease; cyclophilin B; human.

XX OS Homo sapiens.

XX PN EP1074267-A1.

XX PD 07-FEB-2001.

XX PF 24-JUL-2000; 2000EP-0306263.

XX PR 22-JUL-1999; 99JP-0207687.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PI Takasu H, Gotoh M, Yamaoka T;

XX WPI: 2001-193144/20.

XX PT Use of antigenic proteins, peptides, interferon or their encoding DNA,
 in the manufacture of an agent for the induction of antigen-specific T
 cells

XX PS Disclosure: Page 19; 25pp; English.

XX CC This invention describes the novel use of interferons (IFNs) or DNAs
 capable of expressing the interferons and/or antigenic proteins (AP),
 antigenic peptides derived from the proteins or DNAs capable of
 expressing the antigenic proteins or peptides, in the manufacture of
 an agent for induction of antigen-specific T cells. The products of
 the invention have virucide and cytostatic activity and can be used for
 gene therapy or as inducers of antigen-specific T cells. The action of
 interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
 T cell (CTL) by administering an antigenic peptide in an incomplete
 Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
 DNA encoding IFNs) are useful in the manufacture of a medicament for
 inducing antigen-specific T cells in an individual who has been
 administered with AP (or DNA encoding AP) or vice versa. The medicament
 is useful for the treatment or prophylaxis of a tumor or a viral
 infectious disease.

XX SQ Sequence 9 AA;

Query Match 93.9%; Score 46; DB 22; Length 9;
 Best Local Similarity 88.9%; Pred. No. 4.3e+05;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KFHVRVVKDF 9
 |::|::|::|::|
 Db 1 kyhrvikdf 9

RESULT 12

AAB56701
 ID AAB56701 standard; Protein; 183 AA.

XX AC AAB56701;

XX DT 13-MAR-2001 (first entry)

XX DE Human prostate cancer antigen protein sequence SEQ ID NO:1279.

XX KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 vulnary; gastrointestinal; nephrotropic; antineoplastic; gynaecological;
 antibacterial; gene therapy; neutral; immune; reproductive; renal;
 gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 wound; infectious disease.

XX OS Homo sapiens.

XX WO200055174-A1.

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XX PD 21-SEP-2000.
XX PF
XX PR 08-MAR-2000; 2000WO-US05988.
XX PR 12-MAR-1999; 99US-0124270.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (ROSE/) ROSEN C A.
XX PI Rosen CA, Ruben SM;
XX WPI; 2000-587513/55.
XX N-PSDB; AAF15904.
XX PT prostate cancer associated gene sequences, referred to as prostate
XX PT cancer antigens, useful for treatment, prevention, and diagnosis of
XX PT disorders such as prostate cancer.
XX PS Claim 11; Page 1699-1700; 2338pp; English.
XX CC AAF15566 to AAF16505 encode the human prostate cancer associated
XX CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
XX CC The prostate cancer antigens can have neuroprotective, cytostatic,
XX CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
XX CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
XX CC and can be used in gene therapy. The prostate cancer antigen
XX CC polynucleotides may be used for detection of prostate cancer, chromosome
XX CC identification, as chromosome markers, and for numerous other diagnostic
XX CC or research purposes. The prostate cancer antigens may be used to treat
XX CC disorders such as neural, immune, muscular, reproductive,
XX CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
XX CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
XX CC AAB57303 represent sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 183 AA;

Query Match 89.8%; Score 44; DB 21; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIKDF 9
DB 71 fhrvikdf 78

RESULT 13
AAR32353
ID AAR32353 standard; Protein; 212 AA.
XX AC AAR32353;
XX DT 16-JUN-1993 (first entry)
XX DE Cyclophilin C.
XX KW Cyclophilin C; bone marrow; stromal cell line; AC 6; interleukin-1;
XX KW IL-1; cyp A; cyp B; peptidyl-prolyl isomerase; PPIase;
XX KW cyclosporin A; CsA; ligand; calcineurin.
XX OS Mus musculus.
XX PN W09303050-A.
XX PD 18-FEB-1993.
XX PF 05-AUG-1992; 92WO-US06462.
XX PR 05-AUG-1991; 91US-0740375.
XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.

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XX PI Friedman JS, Weissman IL;
XX WPI; 1993-076431/09.
XX N-PSDB; AAQ36841.
XX PT Cyclophilin C polypeptide and nucleic acid encoding it - useful
XX PT for screening a tissue-specific immunosuppressive agent
XX PS Claim 9; Page 46 + Fig 1; 63pp; English.
XX CC A third mammalian cyclophilin, cyp C, was isolated from a cDNA
XX CC library prep. from the murine bone marrow derived stromal cell line
XX CC AC 6. This cDNA was isolated from a substracted sub-library contg.
XX CC genes induced by treatment of the stromal cell line with interleukin-
XX CC 1 (IL-1). The message levels for cyp C show a 2-3 fold induction by
XX CC treatment with IL-1, and this cDNA exhibits a high level of homology
XX CC with known cyclophilins. Cyp C is distinct from mammalian
XX CC cyclophilins A and B in both sequence and tissue distribution of
XX CC expression. A fusion protein contg., e.g. amino acids 16-212 of cyp C
XX CC possesses peptidyl-prolyl isomerase (PPIase) activity which can be
XX CC completely inhibited by addition of cyclosporin A (CsA). These cyp C
XX CC fusion proteins can be used as ligands for the identification of
XX CC intracellular proteins which together form high affinity associations.
XX CC For example, the cyp C fusion protein binds to a protein of 77 kD in
XX CC the absence of CsA, while in the presence of CsA it no longer binds
XX CC to this p77, but instead binds specifically to a protein of 55 kD,
XX CC identified as calcineurin (U.S.N.07/740175).
XX SQ Sequence 212 AA;

Query Match 89.8%; Score 44; DB 14; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIKDF 9
DB 87 fhrvikdf 94

RESULT 14
AAQ92048
ID AAQ92048 standard; Protein; 212 AA.
XX AC AAQ92048;
XX DT 01-AUG-2000 (first entry)
XX DE A. niger peptidyl-prolyl cis-trans isomerase (CYPB).
XX KW Cyclophilin-like peptidyl prolyl cis-trans isomerase; CYPB;
XX KW food processing; Endoplasmic retention signal; cis-trans isomerization;
XX KW protein secretion; toxin; ADP-glucose pyrophosphorylase; glucanase;
XX KW beta-1,4-endoglucanase.
XX OS Aspergillus niger.
XX PH Key Location/Qualifiers
XX FT Peptide 1..23 /label= signal_peptide
XX FT Protein 24..212 /label= mature_protein
XX PN W0200018934-A1.
XX PD 06-APR-2000.
XX PF 30-SEP-1999; 99WO-IB01669.
XX PR 30-SEP-1998; 98GB-0021198.
XX PA (DANI-) DANISCO AS.

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XX Derkx PMF, Madrid SM;
PI WPI: 2000-293167/25.
XX N-PSDB: AAA08772.
DR
XX
XX New peptidyl prolyl cis-trans isomerase, designated CYPB, from
PT Aspergillus niger, useful in methods for increasing the yield of
PT secreted polypeptides, such as enzymes used in food processing, from
PT cells
XX
XX Claim 13; Page 47-48; 52pp; English.
PS
XX
XX This sequence shows Aspergillus niger cyclophilin-like peptidyl prolyl
CC cis-trans isomerase (CYPB). CYPB is capable of catalyzing the cis-trans
CC isomerization of a peptide bond on the N-terminal side of proline
CC residues in polypeptides. CYPB are useful in methods for increasing the
CC yield of secreted polypeptides from cells. The secreted polypeptides may
CC be enzymes (such as chymosin, thaumatocin or alpha-galactosidase) that can
CC be used in food processing, a pest toxin, adenosine diphosphate
CC (ADP)-glucose pyrophosphorylase, a glucanase or beta-1,4-endoglucanase.
XX
XX
SQ Sequence 212 AA;

Query Match 89.8%; Score 44; DB 21; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FHRVIKDF 9
Db 84 fhrvikdf 91
|||||||

RESULT 15
AAG16463
ID AAG16463 standard; Protein: 252 AA.
XX
XX AAG16463;
AC
XX
XX 17-OCR-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 17119.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.

104-MAY-1999; 99US-0132484.
105-MAY-1999; 99US-0132485.
106-MAY-1999; 99US-0132486.
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114-MAY-1999; 99US-0134256.
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114-MAY-1999; 99US-0134370.
118-MAY-1999; 99US-0134768.
119-MAY-1999; 99US-0134941.
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124-MAY-1999; 99US-0135629.
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127-MAY-1999; 99US-0136392.
128-MAY-1999; 99US-0136782.
101-JUN-1999; 99US-0137222.
103-JUN-1999; 99US-0137528.
104-JUN-1999; 99US-0137502.
107-JUN-1999; 99US-0137724.
108-JUN-1999; 99US-0138094.
110-JUN-1999; 99US-0138540.
110-JUN-1999; 99US-0138847.
114-JUN-1999; 99US-0139119.
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118-JUN-1999; 99US-0139461.
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118-JUN-1999; 99US-0139463.
118-JUN-1999; 99US-0139750.
118-JUN-1999; 99US-0139763.
121-JUN-1999; 99US-0139817.
122-JUN-1999; 99US-0139899.
123-JUN-1999; 99US-0140353.
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124-JUN-1999; 99US-0140695.
128-JUN-1999; 99US-0140823.
129-JUN-1999; 99US-0140931.
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101-JUL-1999; 99US-0141842.
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106-JUL-1999; 99US-0142390.
108-JUL-1999; 99US-0142803.
109-JUL-1999; 99US-0142920.
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113-JUL-1999; 99US-0143542.
114-JUL-1999; 99US-0143624.
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119-JUL-1999; 99US-0144333.
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121-JUL-1999; 99US-0144814.
121-JUL-1999; 99US-0145086.
121-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145931.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 14-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 21-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.

PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160981.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 28-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161970.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 87.8%; Score 43; DB 21; Length 252;
Best Local Similarity 87.5%; Pred. No. 0.72;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FHRVIKDF 9
|||:||||
Db 136 fhriikdf 143

Search completed: January 15, 2002, 13:05:26
Job time: 197 sec

GenCore version 4.5
Copyright (C) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2002, 13:16:24 ; Search time 78.85 Seconds
(without alignments)
16.696 Million cell updates/sec

Title: US-09-720-469-2
Perfect score: 50
Sequence: 1 DFMIOGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	50	100.0	167	5	O15729
2	50	100.0	173	10	O9FW22
3	50	100.0	177	4	O43447
4	50	100.0	177	11	O9C007
5	50	100.0	179	5	O26994
6	50	100.0	183	5	O9V989
7	50	100.0	188	11	O9D868
8	50	100.0	203	3	Q01490
9	50	100.0	204	5	O62190
10	50	100.0	205	5	O9W227
11	50	100.0	208	11	O88541
12	50	100.0	210	5	O9U605
13	50	100.0	210	5	Q27716
14	50	100.0	214	3	O94190
15	50	100.0	216	4	O9BVK5
16	50	100.0	216	11	O9DCY1
17	50	100.0	220	5	O44073
18	50	100.0	226	3	O93826
19	50	100.0	231	10	O9AQU0

20	50	100.0	259	10	O9FY98
21	50	100.0	259	10	O9ASS6
22	50	100.0	260	10	O9FPH5
23	49	98.0	185	5	O9GP41
24	49	98.0	752	11	O55035
25	49	98.0	754	4	Q13427
26	48	96.0	162	3	O93970
27	48	96.0	165	3	O9HFU2
28	48	96.0	215	3	O9HFU3
29	46	92.0	104	13	O98UE5
30	46	92.0	172	5	O46022
31	45	90.0	112	10	O65191
32	45	90.0	145	10	O9ATC5
33	45	90.0	147	5	O9N717
34	45	90.0	162	5	O00845
35	45	90.0	171	2	P73789
36	45	90.0	177	5	O02614
37	45	90.0	178	3	O9Y7F6
38	45	90.0	187	5	O909R3
39	45	90.0	188	5	O96878
40	45	90.0	197	5	O9TW32
41	45	90.0	213	5	O96877
42	45	90.0	223	5	O94611
43	45	90.0	295	5	O9U186
44	44	88.0	156	5	O9N1G2
45	44	88.0	166	11	O9D0W5

ALIGNMENTS

RESULT 1

O15729
ID O15729 PRELIMINARY: PRT: 167 AA.
AC O15729;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLOPHILIN (EC 5.2.1.8).
GN CYPL.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HM1;IMSS;
RA Carrero J.C., Petrossian P., Acosta-Camarena E., Ostoa-Saloma P., Ortiz-Ortiz L., Laclette J.P.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HM1;IMSS;
RA Carrero J.C., Petrossian P., Acosta-Camarena E., Ostoa-Saloma P., Ortiz-Ortiz L., Laclette J.P.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FAMILY.
CC EMBL; AF017993; AAB86601.1; -.
DR HSP; P05092; 2CPL.
DR InterPro; IPR002130; CSA_PPase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSA_PPTSMRASE.
DR PROSITE; PS00170; CSA_PPase_1; 1.
DR PROSITE; PS00072; CSA_PPase_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 167 AA; 18139 MW; DBA23FE5BB3290B2 CRC64;

Query Match 100.0%; Score 50; DB 5; Length 167;

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Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
Db 61 DFMIOGGDF 69

RESULT 2
Q9FW22 ID Q9FW22 PRELIMINARY; PRT; 173 AA.
AC Q9FW22;
DT 01-WAR-2001 (TRENBLrel. 16, Created)
DT 01-WAR-2001 (TRENBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE SIMILAR TO ARABIDOPSIS THALIANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
DE (P34791) (FRAGMENT).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
RA Chen C.-S., Shaw J.-F.;
RL "Oryza sativa PAC P0036b10 genomics sequence, complete sequence.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC073405; AAG03106.1; -.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
DR NON_TER 173 173
SQ SEQUENCE 173 AA; 19158 MW; 28EAD80F4625EB9 CRC64;

Query Match 100.0%; Score 50; DB 10; Length 173;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
Db 92 DFMIOGGDF 100

RESULT 3
O43447 ID O43447 PRELIMINARY; PRT; 177 AA.
AC O43447;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE U-SNRNP-ASSOCIATED CYCLOPHILIN (EC 5.2.1.8).
GN USA-CYP OR CYP-20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Horowitz D.S., Kobayashi R., Krainer A.R.;
RC MEDLINE=98067393; PubMed=9404889;
RA Horowitz D.S., Kobayashi R., Krainer A.R.;
RT "A new cyclophilin and the human homologues of yeast Prp3 and Prp4
RL form a complex associated with U4/U6 snRNPs.";
RN [2]
RA Lane W.S., Marahiel M., Luhrmann R.;
RX MEDLINE=98230239; PubMed=9570313;
RA Traigelkamp S., Achsel T., Mundt C., Gethel S.F., Cronshagen U.,
RA Lane W.S., Marahiel M., Luhrmann R.;
RT "The 20kD protein of human [U4/U6.05] trl-snRNPs is a novel

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cyclophilin that forms a complex with the U4/U6-specific 60kD and 90kD
proteins.";
RL RNA 4.127-141(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-CHORIOCARCINOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; AF016371; AAC51927.1; -.
DR EMBL; AF036331; AAC60793.1; -.
DR EMBL; BC003412; AAH03412.1; -.
DR HSSP; P05092; 2RMC.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 177 AA; 19208 MW; 566BCE6361E0F339 CRC64;

Query Match 100.0%; Score 50; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
Db 71 DFMIOGGDF 79

RESULT 4
Q9CQ07 ID Q9CQ07 PRELIMINARY; PRT; 177 AA.
AC Q9CQ07;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE 4833408FLIRIK PROTEIN (I100001J08RIK PROTEIN).
GN 4833408FLIRIK OR I100001J08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=HEAD, EMBRYO, AND CEREBELLUM;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana S.,
RA Saito K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Caasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.N., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momboerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

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CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 CC FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 CC TRANS ISOMERASE FAMILY.
 DR EMBL: AK014665; BAB29493.1; -
 DR EMBL: AK003179; BAB22623.1; -
 DR EMBL: AK005202; BAB23880.1; -
 DR MGD: MGI:1913351; 1100001J08Rik.
 DR MGD: MGI:1921150; 4833408F11Rik.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS00072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 177 AA; 19208 MW; 566BCE6361E0F339 CRC64;

Query Match 100.0%; Score 50; DB 11; Length 177;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPMIOGGDF 9
 DB 71 DPMIOGGDF 79

RESULT 5
 Q26994 ID Q26994 PRELIMINARY; PRT; 179 AA.
 AC Q26994;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
 OS Toxoplasma gondii.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Sarcocystidae;
 OC Toxoplasma.
 OX NCBI_TaxID=5811;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-33.
 RC STRAIN=RH;
 RX MEDLINE=94119329; PubMed=8132648;
 RA High K.P., Joiner K.A., Handschumacher R.E.;
 RT "Isolation, cDNA sequences, and biochemical characterization of the
 RT major cyclosporin-binding proteins of Toxoplasma gondii.";
 RL J. Biol. Chem. 269:9105-9112(1994).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME OF
 CC ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 DR EMBL: U04633; AAA1797.1; -
 DR HSP; P05092; 2CPL.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS00072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Multigene family; Signal.
 FT CHAIN
 SQ SEQUENCE 179 AA; 19652 MW; DB392502CC0DB6CE CRC64;

Query Match 100.0%; Score 50; DB 5; Length 179;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPMIOGGDF 9
 DB 73 DPMIOGGDF 81

RESULT 6
 Q9V9B9 ID Q9V9B9 PRELIMINARY; PRT; 183 AA.
 AC Q9V9B9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CG17266 PROTEIN.
 GN CG17266.

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M., M.G.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003789; AAF57375.1; -
 DR HSP; P05092; 2CPL.
 DR FlyBase: FBgn0033089; CG17266.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00072; CSA_PPIASE_2; 1.
 SQ SEQUENCE 183 AA; 20182 MW; 19E5CE187CB9E949 CRC64;

Query Match 100.0%; Score 50; DB 5; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.039;

Matches	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	DFMIQGGDF 9							
Db	77	DFMIQGGDF 85							
RESULT	7								
Q9D868									
ID	Q9D868	PRELIMINARY;	PRT;	188	AA.				
AC	Q9D868								
DT	01-JUN-2001	(Tremblrel. 17, Created)							
DT	01-JUN-2001	(Tremblrel. 17, Last sequence update)							
DT	01-JUN-2001	(Tremblrel. 17, Last annotation update)							
DE	2010111815RIK	PROTEIN.							
GN	2010111815RIK								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;								
RX	MEDLINE=21085660; PubMed=11217851;								
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,								
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,								
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,								
RA	Saito T., Okazaki Y., Gotohori T., Bono H., Kasakawa T., Saito R.,								
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,								
RA	Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,								
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,								
RA	Sakral L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,								
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,								
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,								
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,								
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,								
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,								
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,								
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,								
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,								
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,								
RA	Hayashizaki Y.;								
RT	*Functional annotation of a full-length mouse cDNA collection.*;								
RL	Nature 409:685-690(2001).								
CC	-1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE								
CC	FOLDING OF PROTEINS (BY SIMILARITY).								
CC	-1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC								
CC	PEPTIDE BONDS IN OLIGOPEPTIDES.								
CC	-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-								
CC	TRANS ISOMERASE FAMILY.								
DR	EMBL: AK008394; BAB25645.1; ..								
DR	MCD; MGI:1919313; 2010111815RIK.								
DR	InterPro: IPR002130; CSA_PPIase.								
DR	Pfam: PF00160; pro_isomerase; 1.								
DR	PRINTS; PR00153; CSAPPISMRASE.								
DR	PROSITE; PS00170; CSA_PPIASE_1; 1.								
DR	PROSITE; PS00072; CSA_PPIASE_2; 1.								
KW	Isomerase; Rotamase.								
SQ	SEQUENCE 188 AA; 20464 MW; ELID29067BA98101 CRC64;								
Query Match	100.0%;	Score 50;	DB 11;	Length 188;					
Best Local Similarity	100.0%;	Pred. No. 0.04;							
Matches	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	DFMIQGGDF 9							
Db	71	DFMIQGGDF 79							
RESULT	8								
Q01490									
ID	Q01490	PRELIMINARY;	PRT;	203	AA.				

AC	Q01490;								
DT	01-NOV-1998	(Tremblrel. 08, Created)							
DT	01-NOV-1998	(Tremblrel. 08, Last sequence update)							
DT	01-JUN-2001	(Tremblrel. 17, Last annotation update)							
DE	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)								
DE	(CYCLOPHILIN B) (ROTAMASE).								
GN	CYPB.								
OS	Orpinomyces sp. PC-2.								
OC	Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;								
OC	Neocallimastixaceae; Orpinomyces.								
OX	NCBI_TaxID=50059;								
RN	[1]								
RP	SEQUENCE FROM N.A.; AND SEQUENCE OF 23-52.								
RX	MEDLINE=95223986; PubMed=7708690;								
RA	Chen H., Li X.-L., Ljungdahl L.G.;								
RT	"A cyclophilin from the polycentric anaerobic rumen fungus Orpinomyces								
RT	sp. strain PC-2 is highly homologous to vertebrate cyclophilin B.";								
RL	Proc. Natl. Acad. Sci. U.S.A. 92:2587-2591(1995).								
CC	-1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.								
CC	-1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC								
CC	PEPTIDE BONDS IN OLIGOPEPTIDES.								
CC	-1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.								
CC	-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).								
CC	-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.								
DR	EMBL: U17900; AAD04195.1; ..								
DR	HSP; P23284; ICDN.								
DR	Mendel; 20786; Unkp;1040;20786.								
DR	InterPro: IPR002130; CSA_PPIase.								
DR	Pfam: PF00160; pro_isomerase; 1.								
DR	PRINTS; PR00153; CSAPPISMRASE.								
DR	PROSITE; PS00170; CSA_PPIASE_1; 1.								
DR	PROSITE; PS00072; CSA_PPIASE_2; 1.								
DR	Isomerase; Rotamase; Signal; Cyclosporin; Endoplasmic reticulum.								
KW	SIGNAL	1	22						
FT	CHAIN	23	203						
FT	BINDING	147	147						
FT	SITE	200	203						
FT	SIMILARITY								
SQ	SEQUENCE 203 AA; 21969 MW; A5748C943058B8E0 CRC64;								
Query Match	100.0%;	Score 50;	DB 3;	Length 203;					
Best Local Similarity	100.0%;	Pred. No. 0.044;							
Matches	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	DFMIQGGDF 9							
Db	85	DFMIQGGDF 93							
RESULT	9								
O62190									
ID	O62190	PRELIMINARY;	PRT;	204	AA.				
AC	O62190;								
DT	01-AUG-1998	(Tremblrel. 07, Created)							
DT	01-AUG-1998	(Tremblrel. 07, Last sequence update)							
DT	01-JUN-2001	(Tremblrel. 17, Last annotation update)							
DE	CYP-5 PROTEIN (EC 5.2.1.8).								
GN	CYP-5.								
OS	Caenorhabditis elegans.								
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;								
OC	Rhabditidae; Peloderinae; Caenorhabditis.								
OX	NCBI_TaxID=6239;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Collage A.;								
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.								
RL	[2]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=94150718; PubMed=7906398;								
RA	Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,								
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,								
RA	Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,								

RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.*;
 RL Nature 368:32-38(1994).
 CC -!- FOLDING: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 CC FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 CC TRANS ISOMERASE FAMILY.
 DR EMBL; Z92784; CAB07192.1; -;
 DR HSP; P23284; ICYN
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 204 AA; 21927 MW; 6216192BFE1FB493 CRC64;

Query Match 100.0%; Score 50; DB 5; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIQGGDF 9
 |||||
 DB 84 DFMIQGGDF 92

RESULT 10
 Q9W227 PRELIMINARY; PRT; 205 AA.
 AC Q9W227;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE CG2852 PROTEIN.
 GN CG2852.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Cocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Workman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Garfield A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT *The genome sequence of Drosophila melanogaster.*;
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 CC FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 CC TRANS ISOMERASE FAMILY.
 CC EMBL; AE003458; AAF46873.1; -;
 DR HSP; P23284; ICYN
 DR FlyBase: FBgn0034753; CG2852.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 205 AA; 22199 MW; A9CFE88B1CC813F7 CRC64;

Query Match 100.0%; Score 50; DB 5; Length 205;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIQGGDF 9
 |||||
 DB 84 DFMIQGGDF 92

RESULT 11
 O88541 PRELIMINARY; PRT; 208 AA.
 ID O88541
 AC O88541;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE CYCLOPHILIN B (EC 5.2.1.8).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR-KYOTO; TISSUE=KIDNEY;
 RA Kainer D.B., Doris P.A.;
 RT "Cyclophilin B";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 CC FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 CC TRANS ISOMERASE FAMILY.
 CC EMBL; AF071225; AAC25590.1; -;
 DR HSP; P23284; ICYN
 DR InterPro: IPR002130; CSA_PPIase.

DR Pfam: PF00160; pro-isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS00072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 208 AA; 22802 MW; 02408DFA7157218C CRC64;

Query Match 100.0%; Score 50; DB 11; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
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 DB 91 DFMIOGGDF 99

RESULT 12
 Q906U5 ID Q906U5 PRELIMINARY; PRT; 210 AA.
 AC Q906U5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYCLOPHILIN.
 GN CYPPL.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FC1/HN;
 RA Li X.R., Yu X.B., Luo S.H., Shan Z.X., Fang J.M., Xu J.;
 RT "Sequence of cyclophilin (cyppl) gene of Plasmodium falciparum
 (isolate FC1/HN).";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 TRANS ISOMERASE FAMILY.
 CC EMBL: AF177281; AAD55769.1; -.
 DR HSP: P05092; 2CPL.
 DR InterPro: IPR002130; CSA_PPIase.
 DR InterPro: IPR002114; PTS_HPR_ser.
 DR Pfam: PF00160; pro-isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS00072; CSA_PPIASE_2; 1.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 210 AA; 24049 MW; 778A31CE0FD47D26 CRC64;

Query Match 100.0%; Score 50; DB 5; Length 210;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
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 DB 101 DFMIOGGDF 109

RESULT 13
 Q27716 ID Q27716 PRELIMINARY; PRT; 210 AA.
 AC Q27716;
 DT 01-JAN-1999 (TREMBLrel. 09, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).

CYP
 OS Plasmodium falciparum (isolate 3D7), and
 OS Plasmodium falciparum (isolate bd2), and
 OS Plasmodium falciparum (isolate hb3).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329, 57267, 137071;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96123383; PubMed=8577319;
 RA Reddy G.R.;
 RT "Cloning and characterization of a Plasmodium falciparum cyclophilin
 gene that is stage-specifically expressed";
 RL Mol. Biochem. Parasitol. 73:111-122(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94052193; PubMed=8234327;
 RA Reddy G.R., Chakrabarti D., Schuster S.M., Perl R.J., Almira E.C.,
 Dame J.B.;
 RT "Gene sequence tags from Plasmodium falciparum genomic DNA fragments
 prepared by the 'genease' activity of mung bean nuclease";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:9867-9871(1993)
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN ALL ERYTHROCYTIC STAGES, BUT
 HIGHEST LEVEL OF EXPRESSION IN THE LATE-RING STAGE.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC EMBL: U10322; AAC46975.1; -.
 DR HSP: P05092; 2CPL.
 DR InterPro: IPR002130; CSA_PPIase.
 DR InterPro: IPR002114; PTS_HPR_ser.
 DR Pfam: PF00160; pro-isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS00072; CSA_PPIASE_2; 1.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 KW Malaria; Cyclosporin; Isomerase; Rotamase; Signal.
 FT SIGNAL 1 39 POTENTIAL.
 FT CHAIN 40 210 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
 FT BINDING 163 163 CSA (POTENTIAL).
 SQ SEQUENCE 210 AA; 24049 MW; 778A359FD47D26 CRC64;

Query Match 100.0%; Score 50; DB 5; Length 210;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
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 DB 101 DFMIOGGDF 109

RESULT 14
 O94190 ID O94190 PRELIMINARY; PRT; 214 AA.
 AC O94190;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYCLOPHILIN B (EC 5.2.1.8).
 GN CYPB.
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes.
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Joseph J.D., Means A.R.;
 RT "Aspergillus nidulans cyclophilin B gene (cypB).";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 FOLDING OF PROTEINS (BY SIMILARITY).

CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; AF107254; AADI7998.1; -.
DR HSSP; P23284; ICYN.
DR InterPro; IPR002130; CSA_PPIase.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Isomerase; Rotamase.
SQ SEQUENCE 214 AA; 23406 MW; 5A4DCFAEBE529DFA CRC64;

Query Match 100.0%; Score 50; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
Db 89 DFMIOGGDF 97

RESULT 15
Q9BVK5 PRELIMINARY; PRT; 216 AA.
AC Q9BVK5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKIN, AND MELANOMA;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001125; AAH01125.1; -.
KW Isomerase.
SQ SEQUENCE 216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;

Query Match 100.0%; Score 50; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
Db 99 DFMIOGGDF 107

Search completed: January 15, 2002, 13:16:25
Job time: 656 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:03:58 ; Search time 37.64 Seconds
(without alignments)
5.381 Million cell updates/sec

Title: US-09-720-469-2
Perfect score: 50
Sequence: 1 DFMIQGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	126	2	US-08-482-728A-10
2	50	100.0	208	1	US-08-142-897-7
3	50	100.0	212	1	US-08-142-897-5
4	48	96.0	126	2	US-08-482-728A-16
5	48	96.0	162	1	US-08-142-897-9
6	48	96.0	162	1	US-08-145-995A-14
7	48	96.0	162	2	US-08-451-747-14
8	48	96.0	162	3	US-09-134-852-14
9	45	90.0	134	2	US-08-482-728A-14
10	45	90.0	176	1	US-08-145-995A-3
11	45	90.0	176	1	US-08-145-995A-4
12	45	90.0	176	2	US-08-451-747-3
13	45	90.0	176	2	US-08-451-747-4
14	45	90.0	176	3	US-09-134-852-3
15	45	90.0	176	3	US-09-134-852-4
16	45	90.0	269	4	US-09-028-366-6
17	45	90.0	591	1	US-08-145-995A-21
18	45	90.0	591	3	US-08-451-747-21
19	45	90.0	591	3	US-09-134-852-21
20	44	88.0	126	2	US-08-482-728A-11
21	44	88.0	134	2	US-08-482-728A-13
22	44	88.0	148	1	US-08-145-995A-6
23	44	88.0	148	2	US-08-451-747-6
24	44	88.0	148	3	US-09-134-852-6
25	44	88.0	175	1	US-08-145-995A-5
26	44	88.0	175	2	US-08-451-747-5
27	44	88.0	175	3	US-09-134-852-5

28 44 88.0 205 1 US-08-142-897-6 Sequence 6, Appli
29 43 86.0 171 4 US-09-028-366-7 Sequence 7, Appli
30 42 84.0 169 1 US-08-145-995A-7 Sequence 7, Appli
31 42 84.0 169 2 US-08-451-747-7 Sequence 7, Appli
32 42 84.0 169 3 US-09-134-852-7 Sequence 7, Appli
33 40 80.0 109 1 US-08-145-995A-15 Sequence 15, Appli
34 40 80.0 109 2 US-08-451-747-15 Sequence 15, Appli
35 40 80.0 109 3 US-09-134-852-15 Sequence 15, Appli
36 40 80.0 126 2 US-08-482-728A-15 Sequence 15, Appli
37 40 80.0 165 1 US-08-145-995A-11 Sequence 11, Appli
38 40 80.0 165 2 US-08-451-747-11 Sequence 11, Appli
39 40 80.0 165 3 US-09-134-852-11 Sequence 11, Appli
40 39 78.0 16 2 US-08-658-639-7 Sequence 7, Appli
41 39 78.0 16 4 US-08-944-604-7 Sequence 7, Appli
42 39 78.0 127 2 US-08-482-728A-9 Sequence 9, Appli
43 39 78.0 141 2 US-08-658-639-14 Sequence 14, Appli
44 39 78.0 141 4 US-08-944-604-14 Sequence 14, Appli
45 39 78.0 161 1 US-08-145-995A-13 Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-08-482-728A-10
; Sequence 10, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482.728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO.: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-482-728A-10

Query Match 100.0%; Score 50; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIQGGDF 9

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Db 42 DFMIQGGDF 50
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RESULT 2
US-08-142-897-7
; Sequence 7, Application US/08142897
; Patent No. 5447852
; GENERAL INFORMATION:
; APPLICANT: Friedman, Jeffrey S.
; APPLICANT: Weissman, Irving L.
; TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tracy J. Dunn
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,897
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/005,917
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,375
; FILING DATE: 05-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy D.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 5490A-92-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-897-7

Query Match 100.0%; Score 50; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
Db 91 DFMIQGGDF 99
|||||
RESULT 3
US-08-142-897-5
; Sequence 5, Application US/08142897
; Patent No. 5447852
; GENERAL INFORMATION:
; APPLICANT: Friedman, Jeffrey S.
; APPLICANT: Weissman, Irving L.
; TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tracy J. Dunn
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,897
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/005,917
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,375
; FILING DATE: 05-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy D.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 5490A-92-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-897-5

Query Match 100.0%; Score 50; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
Db 93 DFMIQGGDF 101
|||||
RESULT 4
US-08-482-728A-16
; Sequence 16, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
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; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-482-728A-16

Query Match 96.0%; Score 48; DB 2; Length 126;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
Db 42 DFMLQGGDF 50

RESULT 5
US-08-142-897-9
; Sequence 9, Application US/08142897
; Patent No. 5447852
; GENERAL INFORMATION:
; APPLICANT: Friedman, Jeffrey S.
; APPLICANT: Weissman, Irving L.
; TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tracy J. Dunn
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,897
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/005,917
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,375
; FILING DATE: 05-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy D.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 5490A-92-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-142-897-9

Query Match 96.0%; Score 48; DB 1; Length 162;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
Db 57 DFMLQGGDF 65

RESULT 6
US-08-145-995A-14
; Sequence 14, Application US/08145995A
; Patent No. 5482850
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,995A
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-145-995A-14

Query Match 96.0%; Score 48; DB 1; Length 162;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
Db 57 DFMLQGGDF 65

RESULT 7
US-08-451-747-14
; Sequence 14, Application US/08451747
; Patent No. 5821107
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY

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;; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
;; STREET: 32 TOZER ROAD
;; CITY: BEVERLY
;; STATE: MASSACHUSETTS
;; COUNTRY: USA
;; ZIP: 01915
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/08/451,747
;; APPLICATION NUMBER: US/08/451,747
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/145,995
;; FILING DATE: 29-OCT-1993
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WILLIAMS, GREGORY D.
;; REGISTRATION NUMBER: 30901
;; REFERENCE/DOCKET NUMBER: NEB-046-DIV
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (508) 927-5054
;; TELEFAX: (508) 927-1705
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 162 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-451-747-14

Query Match 96.0%; Score 48; DB 2; Length 162;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
Db 57 DFMLQGGDF 65

RESULT 8
US-09-134-852-14
;; Sequence 14, Application US/09134852
;; Patent No. 6127148
;; GENERAL INFORMATION:
;; APPLICANT: CARLOW, CLOTILDE K.S.
;; APPLICANT: PAGE, ANTONY
;; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
;; COMPOUNDS
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;; CUSHMAN
;; STREET: 110 WATER STREET
;; CITY: BOSTON
;; STATE: MASSACHUSETTS
;; COUNTRY: USA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/134,852
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/145,995
;; FILING DATE: 29-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: RESNICK, DAVID S.
;; REGISTRATION NUMBER: 34235
;; REFERENCE/DOCKET NUMBER: 43406
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 523-3400
;; TELEFAX: (617) 523-6440
;; TELEX: 200291 STRE UR
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 162 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-09-134-852-14

Query Match 96.0%; Score 48; DB 3; Length 162;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
Db 57 DFMLQGGDF 65

RESULT 9
US-08-482-728A-14
;; Sequence 14, Application US/08482728A
;; Patent No. 5968802
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Bruce
;; APPLICANT: Fisher, Joseph
;; APPLICANT: Payan, Donald
;; TITLE OF INVENTION: Nuclear Cyclophilin
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Flehr, Hobbach, Test, Albritton
;; ADDRESSEE: & Herbert
;; STREET: Four Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States
;; ZIP: 94111-4187
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/482,728A
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Silva, Robin M.
;; REGISTRATION NUMBER: 38,304
;; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989
;; TELEFAX: (415) 398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 134 amino acids
;; TYPE: amino acid

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; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-482-728A-14

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Query Match          90.0%; Score 45; DB 2; Length 134;
Best Local Similarity 88.9%; Pred. No. 0.36;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DFMIQGGDF 9
Db 50 NFMIQGGDF 58

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RESULT 10
US-08-145-995A-3
; Sequence 3, Application US/08145995A
; Patent No. 5482850
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-145-995A-3

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Query Match          90.0%; Score 45; DB 1; Length 176;
Best Local Similarity 88.9%; Pred. No. 0.48;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DFMIQGGDF 9
Db 70 NFMIQGGDF 78

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RESULT 11
US-08-145-995A-4
; Sequence 4, Application US/08145995A
; Patent No. 5482850

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; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-145-995A-4

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Query Match          90.0%; Score 45; DB 1; Length 176;
Best Local Similarity 88.9%; Pred. No. 0.48;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DFMIQGGDF 9
Db 70 NFMIQGGDF 78

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RESULT 12
US-08-451-747-3
; Sequence 3, Application US/08451747
; Patent No. 5821107
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/451,747
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
PS-08-451-747-3

Query Match 90.0%; Score 45; DB 2; Length 176;
Best Local Similarity 88.9%; Pred. No. 0.48;
Matches 8: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
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Db 70 NFMIQGGDF 78

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-451-747-4

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Query Match 90.0%; Score 45; DB 2; Length 176;
Best Local Similarity 88.9%; Pred. NO. 0.48;
Matches 8; Conservative 1; Mismatches 0; Indels

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Qy      1 DFMIOGGDF 9
        :|||||||
Db      70 NEMIOGGDF 78
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RESULT 14
US-09-134-852-3
: Sequence 3, Application US/09134852
: Patent No. 6127148
: GENERAL INFORMATION:
: APPLICANT: CARLOW, CLOFILDE K. S.
: APPLICANT: PAGE, ANTONY
: TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
: TITLE OF INVENTION: COMPOUNDS
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
: ADDRESSEE: CUSHMAN
: STREET: 130 WATER STREET
: CITY: BOSTON
: STATE: MASSACHUSETTS
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/134,852

Query Match 90.0%; Score 45; DB 3; Length 176;
Best Local Similarity 88.9%; Pred. No. 0.48;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DFMIQGGDF	9
		:	
Db	70	NFMIQGGDF	78

RESULT 15
US-09-134-852-4
; Sequence 4, Application US/09134852
; Patent No. 6127148
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,852
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,995
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-134-852-4

Query Match 90.0%; Score 45; DB 3; Length 176;
Best Local Similarity 88.9%; Pred No. 0.48;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DFMIQGGDF 9
Db 70 NFMIQGGDF 78

Search completed: January 15, 2002, 13:03:58
Job time: 214 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:14:58 ; Search time 24.88 Seconds
(without alignments)
13.263 Million cell updates/sec

Title: US-09-720-469-2

Perfect score: 50

Sequence: 1 DMFIQGGDF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	163	1	CYPB_UROFA
2	50	100.0	183	1	CYPB_CAEEL
3	50	100.0	204	1	CYP5_CAEEL
4	50	100.0	207	1	CYP5_CHICK
5	50	100.0	208	1	CYPB_BOVIN
6	50	100.0	208	1	CYPB_HUMAN
7	50	100.0	208	1	CYPB_MOUSE
8	50	100.0	208	1	CYPB_RAT
9	50	100.0	212	1	CYPC_MOUSE
10	50	100.0	260	1	CYP4_ARATH
11	48	96.0	161	1	CYPH_YEAST
12	48	96.0	165	1	PP1_STRCH
13	46	92.0	171	1	CYP2_CAEEL
14	46	92.0	171	1	CYP7_CAEEL
15	46	92.0	192	1	CYP1_CAEEL
16	45	90.0	173	1	CYP3_CAEEL
17	45	90.0	201	1	CYP6_CAEEL
18	45	90.0	225	1	CYPD_YEAST
19	45	90.0	248	1	CYPB_VICFA
20	45	90.0	843	1	CYP1_BRUMA
21	45	90.0	1453	1	NKCR_MOUSE
22	45	90.0	1462	1	NKCR_HUMAN
23	44	88.0	182	1	CYPC_YEAST
24	44	88.0	205	1	CYPB_YEAST
25	44	88.0	212	1	CYPC_HUMAN
26	44	88.0	215	1	PP1B_TREPA
27	44	88.0	223	1	CYPH_NEUCR
28	44	88.0	370	1	CYP4_BOVIN
29	44	88.0	370	1	CYP4_HUMAN
30	42	84.0	162	1	CYPH_CANAL
31	42	84.0	162	1	CYPH_SCHPO
32	42	84.0	169	1	CYP2_ARATH
33	41	82.0	172	1	CYPH_MAIZE

34	41	82.0	300	1	CYPE_DROME
35	40	80.0	155	1	CYP2_SCHPO
36	40	80.0	164	1	CYPH_BLAG
37	40	80.0	165	1	CYPH_DROME
38	40	80.0	172	1	CYP1_ARATH
39	40	80.0	172	1	CYPH_LUPUL
40	39	78.0	150	1	CYPH_ALICE
41	39	78.0	161	1	CYPH_ECHGR
42	39	78.0	163	1	CYPH_BOVIN
43	39	78.0	163	1	CYPH_CRILO
44	39	78.0	163	1	CYPH_MOUSE
45	39	78.0	163	1	CYPH_RAT

ALIGNMENTS

RESULT 1
CYPH_UROFA
ID CYPH_UROFA STANDARD; PRT; 163 AA.
AC O00060;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (PLANTA-INDUCED RUST
DE PROTEIN 28).
GN PIG28.
OS Uromyces Fungae.
OC Eukaryota; Fungi; Basidiomycota; Urediniomycetes; Urediniomycetidae;
OC Uredinales; Pucciniaceae; Uromyces.
OX NCBI_TaxID=55588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=I2; TISSUE=Haustorium;
RA MEDLINE=97294919; PubMed=9150592;
RX Hahn M., Mendgen K.;
RT "Characterization of in planta-induced rust genes isolated from a
haustorium-specific cDNA library."
RL MOL. Plant Microbe Interact. 10:427-437(1997).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: HAUSTORIA AND RUST-INFECTED LEAVES. ALSO
OBSERVED, IN LOWER LEVELS, IN SPORES OR HYPHAE FORMED IN VITRO.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U81792; BAB39880.1;
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE.1; 1.
DR PROSITE: PS50072; CSA_PPIASE.2; 1.
KW Cyclosporin; Isomerase; Rotamase; Multigene family.
SQ SEQUENCE 163 AA; 17992 MW; A00A641CBA0DBDID CRC64;

Query Match 100.0%; Score 50; DB 1; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DMFIQGGDF 9

CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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 CC -----

DR EMBL; M63553; AAA49004.1; -
 DR PIR; A40516; A40516.
 DR HSSP; P23284; 1CYN.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro-isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 207 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
 FT SITE 198 207 PREVENT SECRETION FROM ER
 FT (BY SIMILARITY).
 FT SEQUENCE 207 AA; 22413 MW; D9C0C2E528E25B59 CRC64;

Query Match 100.0%; Score 50; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 0.0082;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFMIQGGDF 9
 D 90 DFMIQGGDF 98
 |||||

RESULT 5
 CYPB_BOVIN
 ID CYPB_BOVIN STANDARD; PRT; 208 AA.
 AC P80311;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCVLP).
 GN PP1B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Carrello A., Mark P.J., House A.K., Ratajczak T.;
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 26-71.
 RC TISSUE=Brain;
 RX MEDLINE=94283623; PubMed=8013656;
 RA Galat A., Bouet F.;
 RT "Cyclophilin-B is an abundant protein whose conformation is similar
 RT to cyclophilin-A.";
 RL FEBS Lett. 347:31-36(1994).
 RN [3]
 RP SEQUENCE OF 26-45.
 RX MEDLINE=94280416; PubMed=8010972;
 RA Bose S., Muecke M., Freedman R.B.;
 RT "The characterization of a cyclophilin-type peptidyl prolyl
 RT cis-trans-isomerase from the endoplasmic-reticulum lumen.";
 RL Biochem. J. 300:871-875(1994).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC -----
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DR EMBL; D14073; BAA03158.1; -
 DR HSSP; P23284; 1CYN.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro-isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family.
 FT SIGNAL 1 25
 FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
 FT SITE 199 208 PREVENT SECRETION FROM ER.
 FT CONFLICT 30 30 K -> G (IN REF. 3).
 FT SEQUENCE 208 AA; 22701 MW; 0097C88289AF6276 CRC64;

Query Match 100.0%; Score 50; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFMIQGGDF 9
 D 91 DFMIQGGDF 99
 |||||

RESULT 6
 CYPB_HUMAN
 ID CYPB_HUMAN STANDARD; PRT; 208 AA.
 AC P23284;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCVLP) (CYP-S1).
 GN PP1B OR CYPB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-40.
 RX MEDLINE=91156714; PubMed=2000394;
 RA Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,
 RA Walsh C.T.;
 RT "Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-
 RT prolyl isomerase with a signal sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91250363; PubMed=2040592;
 RA Spik G., Haendler B., Delmas O., Mariller C., Chamoux M., Maes P.,
 RA Tartar A., Montreuil J., Stedman K., Kocher H.P., Keller R.,
 RA Hiestand P.C., Movva N.R.;
 RT "A novel secreted cyclophilin-like protein (SCVLP).";
 RL J. Biol. Chem. 266:10735-10738(1991).
 RN [3]
 RP SEQUENCE OF 2-208 FROM N.A.
 RX MEDLINE=91260697; PubMed=1710767;
 RA Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;

RT "An endoplasmic reticulum-specific cyclophilin.";
RL Mol. Cell. Biol. 11:3484-3491(1991).
RN [4]
RP SEQUENCE OF 64-76 AND 151-157.
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [5]
RP SUBCELLULAR LOCATION.
RX MEDLINE=92112948; PubMed=1530944;
RA Arber S., Krause K.H., Caroni P.;
RT "S-cyclophilin is retained intracellularly via a unique COOH-terminal
RT sequence and colocalizes with the calcium storage protein
RT calreticulin.";
RL J. Cell Biol. 116:113-125(1992).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=94255495; PubMed=8197205;
RA Mikol V., Kallen J., Walkinshaw M.D.;
RT "X-ray structure of a cyclophilin B/cyclosporin complex: comparison
RT with cyclophilin A and delineation of its calcineurin-binding
RT domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).
CC -!- FUNCTION: PPTASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPTASE FAMILY.
CC
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CC
CC -----
DR EMBL; M60857; AAA52150.1; -;
DR EMBL; M63573; AAA36601.1; ALT_INIT.
DR EMBL; M60457; AAA35733.1; -;
DR PIR; A39118; CSHUB.
DR PIR; A40515; A40515.
DR PDB; 1CYN; 29-JAN-96.
DR Aarhus/Ghent-2DPAGE; 117; NEPHGE.
DR MIM; 123841; -;
DR InterPro; IPR002130; CSA_PPTase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPTASE_1; 1.
DR PROSITE; PS00170; CSA_PPTASE_1; 1.
DR PROSITE; PS00170; CSA_PPTASE_1; 1.
DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family; 3D-structure.
FT SIGNAL 1 25
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER.
SQ SEQUENCE 208 AA; 22742 MW; A814461B7EBD4579 CRC64;

Query Match 100.0%; Score 50; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIQGGDF 9
DB 91 DFMIQGGDF 99

RESULT 7
CYPB_MOUSE

ID CYPB_MOUSE STANDARD; PRT; 208 AA.
AC P24369;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (BC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCVLP) (CYP-S1).
GN PPIB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91260697; PubMed=1710767;
RA Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
RT "An endoplasmic reticulum-specific cyclophilin.";
RL Mol. Cell. Biol. 11:3484-3491(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RX MEDLINE=92096454; PubMed=1756174;
RA Schumacher A., Schroeter H., Multhaup G., Nordheim A.;
RT "Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a
RT putative signal sequence expressed in differentiating F9 cells.";
RL Biochim. Biophys. Acta 1129:13-22(1991).
CC -!- FUNCTION: PPTASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPTASE FAMILY.
CC
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CC -----
DR EMBL; M60456; AAA37498.1; -;
DR EMBL; X58990; CAA41736.1; -;
DR PIR; B39722; B39722.
DR PIR; S21835; S21835.
DR HSP; P23284; 1CYN.
DR MGD; MGI:97750; Ppib.
DR InterPro; IPR002130; CSA_PPTase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPTASE_1; 1.
DR PROSITE; PS00170; CSA_PPTASE_1; 1.
DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER.
FT (BY SIMILARITY).
SQ SEQUENCE 208 AA; 22713 MW; 4B8DF5AE40BAD3A7 CRC64;

Query Match 100.0%; Score 50; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIQGGDF 9
DB 91 DFMIQGGDF 99

RESULT 8
CYPB_RAT
ID CYPB_MOUSE STANDARD; PRT; 208 AA.

P24368;
 01-MAR-1992 (Rel. 21, Created)
 01-MAR-1992 (Rel. 21, Last sequence update)
 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCVLP) (CYP-S1).
 GN PP1B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90300692; PubMed=2194066;
 RA Iwai N., Inagami T.;
 RT "Molecular cloning of a complementary DNA to rat cyclophilin-like
 protein mRNA.";
 RL Kidney Int. 37:1460-1465(1990).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RX MEDLINE=92112948; PubMed=1530944;
 RA Arber S., Krause K.-H., Caroni P.;
 RT "S-cyclophilin is retained intracellularly via a unique COOH-terminal
 sequence and colocalizes with the calcium storage protein
 calreticulin.";
 RL J. Cell Biol. 116:113-125(1992).
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 DR HSSP; P23284; 1CVN.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 MW Multigene family.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
 FT SITE 199 208 PREVENT SECRETION FROM ER
 (BY SIMILARITY).
 SQ SEQUENCE 208 AA; 23025 MW; 76D12AC3427FEF32 CRC64;
 Query Match 100.0%; Score 50; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DFMIQGGDF 9
 | | | | | | | | | |
 Db 91 DFMIQGGDF 99
 RESULT 9
 CYP_MOUSE
 ID CYP4_MOUSE STANDARD; PRT; 212 AA.
 AC P30412;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
 DE (CYCLOPHILIN C).
 GN PPIC OR CYPB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91347379; PubMed=1652374;

RA Friedman J., Weissman I.L.;
 RT "Two cytoplasmic candidates for immunophilin action are revealed by
 affinity for a new cyclophilin: one in the presence and one in the
 absence of CSA.";
 RL Cell 66:799-806(1991).
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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 CC -----
 DR EMBL; M74227; AAA37511.1;
 DR PIR; A40047; A40047.
 DR HSSP; P05092; 2RMC.
 DR MGD; MGI:97751; Ppic.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Multigene family.
 MW Cyclosporin; 212 AA; 22794 MW; C99E7AA5D0FA04B6 CRC64;
 SQ SEQUENCE 212 AA; 22794 MW; C99E7AA5D0FA04B6 CRC64;
 Query Match 100.0%; Score 50; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DFMIQGGDF 9
 | | | | | | | | | |
 Db 93 DFMIQGGDF 101
 RESULT 10
 CYP4_ARATH
 ID CYP4_ARATH STANDARD; PRT; 260 AA.
 AC P34791;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR
 DE (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING
 DE PROTEIN).
 GN ROC4 OR F21F14.200.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA; TISSUE=Leaf;
 RX MEDLINE=94179146; PubMed=8132503;
 RA Lippuner V., Chou I.T., Scott S.V., Ettinger W.F., Theg S.M.,
 RA Gasser C.S.;
 RT "Cloning and characterization of chloroplast and cytosolic forms of
 cyclophilin from Arabidopsis thaliana.";
 RL J. Biol. Chem. 269:7863-7868(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=98088013; PubMed=9426607;
 RA Chou I.T., Gasser C.S.;
 RT "Characterization of the cyclophilin gene family of Arabidopsis

```

thaliana and phylogenetic analysis of known cyclophilin proteins.*;
Plant Mol. Biol. 35:873-892(1997).
[3]
SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
RA Cholsne N., Robert C., Brottier P., Wincker P., Cattolico L.,
RA Artiguenave F., Saurin W., Weissbach J., Mewes H.-W., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.;
RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
-----
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-----
EMBL; L14845; AAA20048.1; -.
DR EMBL; U42724; AAB96831.1; -.
DR EMBL; AL138642; CAB71910.1; -.
DR HSSP; P23284; ICYN.
DR SWISS-2DPAGE; P34791; ARATH.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS0072; CSA_PPIASE_2; 1.
DR Cyclosporin; Isomerase; Rotamase; Chloroplast; Transit peptide;
KW Multigene family.
FT TRANSIT 1 78 CHLOROPLAST (POTENTIAL).
FT CHAIN 79 260 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
FT SEQUENCE 260 AA; 28208 MW; D412AECB8A5A3B7 CRC64;
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Query Match 100.0%; Score 50; DB 1; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPMIOGGDF 9
Db 150 DPMIOGGDF 158
|||||
150 DPMIOGGDF 158

RESULT 11
CYPH_YEAST STANDARD; PRT; 161 AA.
AC P14832;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (CPH) (PPI-II).
GN CPRI OR CYPI OR CPHI OR SCCI OR YDR153C OR YD8358.10C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=90221831; PubMed=2183184;
RA Dietmeier K., Tropschug M.;
RT "Nucleotide sequence of a full-length cDNA coding for cyclophilin
RT (peptidyl-prolyl cis-trans isomerase) of Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 18:373-373(1990).
[2]

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SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
MEDLINE=90075969; PubMed=2687115;
RA Haendler B., Keller R., Hiestand P.C., Kocher H.P., Wegmann G.,
RA Movva N.R.;
RT "Yeast cyclophilin: isolation and characterization of the protein,
RT cDNA and gene.";
RL Gene 83:39-45(1989).
RN [3]
SEQUENCE FROM N.A.
RA STRAIN=S288C / AB972;
RA Murphy L., Richards C., Harris D., Barrell B.G., Rajandream M.A.,
RA Walsh S.V.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
CHARACTERIZATION, AND PARTIAL SEQUENCE.
RA MEDLINE=93160233; PubMed=8431466;
RA Hasumi H., Nishikawa T.;
RT "Purification and properties of multiple molecular forms of yeast
RT peptidyl prolyl cis-trans isomerase.";
RL Biochim. Biophys. Acta 1161:161-167(1993).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
-----
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-----
EMBL; X17505; CAA35545.1; -.
DR EMBL; M30513; AAA34528.1; -.
DR EMBL; Z50046; CAA90376.1; -.
DR PIR; S25443; CSBY.
DR PIR; S29645; S29645.
DR HSSP; P05092; 3CYS.
DR SGD; S0002562; CPHI.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS0072; CSA_PPIASE_2; 1.
DR Cyclosporin; Isomerase; Rotamase; Multigene family; Acetylation.
KW MOD_MET 1 1 ACETYLATION.
FT INIT_MET 0 0
FT MOD_RES 1 1
SQ SEQUENCE 161 AA; 17259 MW; CE2B71DB8D8C44D7 CRC64;

Query Match 96.0%; Score 48; DB 1; Length 161;
Best Local Similarity 88.9%; Pred. No. 0.016;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPMIOGGDF 9
Db 56 DPMIOGGDF 64
|||||
56 DPMIOGGDF 64

RESULT 12
PPI_STRCH STANDARD; PRT; 165 AA.
AC Q06118;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN HOMOLOG).
OS Streptomyces chrysomallus.

```


OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1899;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 4-41.
 RC STRAIN-ATCC 11523;
 RX MEDLINE=93116593; PubMed=1474897;
 RA Pahl A., Uehlein M., Bang H., Schlumbohm W., Keller U.;
 RT "Streptomycetes possess peptidyl-prolyl cis-trans isomerases that
 strongly resemble cyclophilins from eukaryotic organisms.";
 RL Mol. Microbiol. 6:3551-3558(1992).
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
 CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC
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 CC
 DR EMBL; Z15137; CAA78840.1; -
 DR PIR; S28020; S28020.
 DR HSP; P05092; 3CYS.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 KW Cyclosporin; isomerase; Rotamase.
 SQ SEQUENCE 165 AA; 17716 MW; 2CF1DF725CD6F47D CRC64;

 Query Match 96.0%; Score 48; DB 1; Length 165;
 Best Local Similarity 88.9%; Pred. No. 0.016;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 DFMIOGGDF 9
 |||||
 Db 58 DFMIOGGDF 66

 RESULT 13
 CYP2_CAEL
 ID CYP2_CAEL STANDARD; PRT; 171 AA.
 AC P52010;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 2 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
 DE (CYCLOPHILIN-2).
 GN CYP-2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=96276416; PubMed=8694762;
 RA Page A.P., Macniven K., Hengartner M.O.;
 RT "Cloning and biochemical characterization of the cyclophilin
 homologues from the free-living nematode Caenorhabditis elegans.";
 RL Biochem. J. 317:179-185(1996).
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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 CC
 DR EMBL; U34354; AAC47127.1; -
 DR HSP; P05092; 1ANW.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase; Multigene family.
 SQ SEQUENCE 171 AA; 18416 MW; 23498E7AA437034C CRC64;

 Query Match 92.0%; Score 46; DB 1; Length 171;
 Best Local Similarity 88.9%; Pred. No. 0.041;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 DFMIOGGDF 9
 |||||
 Db 66 DFMIOGGDF 74

 RESULT 14
 CYP7_CAEL
 ID CYP7_CAEL STANDARD; PRT; 171 AA.
 AC P52015;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 7 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
 DE (CYCLOPHILIN-7).
 GN CYP-7 OR Y75H12B.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=96276416; PubMed=8694762;
 RA Page A.P., Macniven K., Hengartner M.O.;
 RT "Cloning and biochemical characterization of the cyclophilin
 homologues from the free-living nematode Caenorhabditis elegans.";
 RL Biochem. J. 317:179-185(1996).
 CC [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA White S.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-13.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=97295299; PubMed=9150941;
 RA Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;
 RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans
 homogenates and identification of protein spots by microsequencing.";
 RL Electrophoresis 18:557-562(1997).
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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CC -----

DR EMBL; U27559; AAC47125.1; -;
DR EMBL; AL032663; CAA21760.1; -;
DR HSSP; P05092; 1AWV; -;
DR WormPep; Y75B12B.2; CE20371;
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1;
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1;
DR PROSITE; PS50072; CSA_PPIASE_2; 1;
DR PROSITE; PS50072; CSA_PPIASE_2; 1;
KW Isomerase; Rotamase; Multigene family.
FT CONFLICT 12 12 I -> T (IN REF. 1).
SQ SEQUENCE 171 AA; 18401 MW; D5BD5E32A32942A7 CRC64;

Query Match 92.0%; Score 46; DB 1; Length 171;
Best Local Similarity 88.9%; Pred. No. 0.041; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 1;
OY 1 DFMIOGGDF 9
Db 66 EFMIOGGDF 74
:|||||

RESULT 15
CYP1L_CAEEL STANDARD; PRT; 192 AA.
AC P52009;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN-1).
GN CYP-1 OR Y49A3A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peleocerinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=96276416; PubMed=8694762;
RA Page A.P., Macniven K., Hengartner M.O.;
RT "Cloning and biochemical characterization of the cyclophilin
RL homologues from the free-living nematode Caenorhabditis elegans.*";
RL Biochem. J. 317:179-185(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA McMurray A.A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; U30943; AAC47116.1; -;
DR EMBL; AL033512; CAA22075.1; -;
DR HSSP; P05092; 1AWV; -;
DR WormPep; Y49A3A.5; CE22213.
DR InterPro; IPR002130; CSA_PPIase.
DR -----

DR Pfam; PF00160; pro_isomerase; 1;
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1;
DR PROSITE; PS50072; CSA_PPIASE_2; 1;
KW Isomerase; Rotamase; Multigene family.
SQ SEQUENCE 192 AA; 20710 MW; C2094D91809ECE85 CRC64;

Query Match 92.0%; Score 46; DB 1; Length 192;
Best Local Similarity 88.9%; Pred. No. 0.047; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 1;
OY 1 DFMIOGGDF 9
Db 84 EFMIOGGDF 92
:|||||

Search completed: January 15, 2002, 13:14:58
Job time: 654 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:06:15 ; Search time 42.04 Seconds
(without alignments)
16.308 Million cell updates/sec

Title: US-09-720-469-2

Perfect score: 50

Sequence: 1 DFMIQGGDF 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	179	2 A53522	peptidylprolyl iso
2	50	100.0	183	2 S71547	peptidylprolyl iso
3	50	100.0	183	2 T18578	peptidylprolyl iso
4	50	100.0	204	2 T21587	peptidylprolyl iso
5	50	100.0	207	2 A40516	peptidylprolyl iso
6	50	100.0	208	1 CSHUB	peptidylprolyl iso
7	50	100.0	212	2 A40047	peptidylprolyl iso
8	50	100.0	215	2 A56861	peptidylprolyl iso
9	50	100.0	260	2 B53422	peptidylprolyl iso
10	49	98.0	754	1 JC5314	cdc28/cdc2-like ki
11	48	96.0	162	1 CSBY	peptidylprolyl iso
12	48	96.0	165	2 S28020	peptidylprolyl iso
13	48	96.0	179	2 JT0686	peptidylprolyl iso
14	46	92.0	171	2 T27371	peptidylprolyl iso
15	46	92.0	172	2 T27882	peptidylprolyl iso
16	46	92.0	192	2 T27034	peptidylprolyl iso
17	45	90.0	171	2 S74880	peptidylprolyl iso
18	45	90.0	173	2 T27373	peptidylprolyl iso
19	45	90.0	201	2 T18573	peptidylprolyl iso
20	45	90.0	225	2 S38324	peptidylprolyl iso
21	45	90.0	248	2 T12056	peptidylprolyl iso
22	45	90.0	1403	1 A47328	peptidylprolyl iso
23	45	90.0	1507	2 B47328	natural killer cel
24	44	88.0	169	2 T29283	natural killer cel
25	44	88.0	173	2 T39632	peptidylprolyl iso
26	44	88.0	180	2 S51457	peptidylprolyl iso
27	44	88.0	182	2 S30507	peptidylprolyl iso
28	44	88.0	201	2 T50837	peptidylprolyl iso
29	44	88.0	201	2 T02489	peptidylprolyl iso

30	44	88.0	205	2 S12324	peptidylprolyl iso
31	44	88.0	212	2 A54204	peptidylprolyl iso
32	44	88.0	215	2 A71261	peptidylprolyl iso
33	44	88.0	223	1 CSNCM	peptidylprolyl iso
34	44	88.0	227	2 S71849	peptidylprolyl iso
35	44	88.0	234	2 T49204	peptidylprolyl iso
36	44	88.0	370	2 A46579	estrogen receptor-
37	44	88.0	370	2 A45981	peptidylprolyl iso
38	43	86.0	196	2 E86736	peptidylprolyl ci
39	43	86.0	199	2 F84808	probable peptidyl-
40	43	86.0	356	2 S62327	probable 40 kd pep
41	42	84.0	162	1 CSZPA	peptidylprolyl iso
42	42	84.0	162	1 CSCK	peptidylprolyl iso
43	42	84.0	169	2 S22496	peptidylprolyl iso
44	42	84.0	204	2 T50838	peptidylprolyl iso
45	42	84.0	331	2 T31517	hypothetical prote

ALIGNMENTS

RESULT 1

A53522

peptidylprolyl isomerase (EC 5.2.1.8) [similarity] - Toxoplasma gondii

N:Contains: cyclophilin

C:Species: Toxoplasma gondii

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-2000

C:Accession: A53522

R:High, K.P.; Joiner, K.A.; Handschumacher, R.E.

J. Biol. Chem. 269, 9105-9112, 1994

A:Title: Isolation, cDNA sequences, and biochemical characterization of the major cyc

A:Reference number: A53522; MUID:94179329

A:Accession: A53522

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-179 <HIG>

A:Cross-references: GB:U04633

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase

F:22-178/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 50; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9

Db 73 DFMIQGGDF 81

RESULT 2

S71547

peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat

N:Alternate names: cyclophilin B; PPIASE

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999

C:Accession: S71547

R:Ruecknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaefer, M.; Fischer, G.

submitted to the Protein Sequence Database, November 1996

A:Reference number: S71547

A:Accession: S71547

A:Molecule type: protein

A:Residues: 1-183 <RUE>

A:Experimental source: liver

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase

F:1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <MAT>

F:10-172/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 50; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.0065;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPMIOGGDF 9

|||||

Db 66 DPMIOGGDF 74

RESULT 3

T18578 peptidylprolyl isomerase (EC 5.2.1.8) cyp-11 [similarity] - Caenorhabditis elegans

N:Contains: cyclophilin

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000

C:Accession: T18578; T24269

R:Page, A.P.; MacNiven, K.

submitted to the EMBL Data Library, August 1995

A:Reference number: Z18986

A:Accession: T18578

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-183 <PAG>

A:Cross-References: EMBL:U34955; PIDN:NAAC47115.1

A:Experimental source: strain Bristol N2

R:Sims, M.

submitted to the EMBL Data Library, October 1995

A:Reference number: Z19867

A:Accession: T24269

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-183 <WIL>

A:Cross-References: EMBL:Z66499; PIDN:CAA91297.1; GSPDB:GN00020; CESP:T01B7.4

A:Experimental source: clone T01B7

C:Genetics:

A:Gene: CESP:cyp-11

A:Map position: 2

A:Introns: 34/3; 87/3; 148/1

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase

F:16-183/Domain: cyclophilin homology <CYP>

Query Match

Best Local Similarity 100.0%; Score 50; DB 2; Length 183;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPMIOGGDF 9

|||||

Db 77 DPMIOGGDF 85

RESULT 4

T21587 peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans

N:Contains: cyclophilin

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000

C:Accession: T21587

R:Cottage, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19446

A:Accession: T21587

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-204 <WIL>

A:Cross-References: EMBL:Z92784; PIDN:CAB07192.1; GSPDB:GN00019; CESP:F31C3.1

A:Experimental source: clone F31C3

C:Genetics:

A:Gene: CESP:F31C3.1

A:Map position: 1

A:Introns: 69/3

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase

F:28-190/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 50; DB 2; Length 204;

Best Local Similarity 100.0%; Pred. No. 0.0073;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPMIOGGDF 9

|||||

Db 84 DPMIOGGDF 92

RESULT 5

A40516

peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999

C:Accession: A40516

R:Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.

J. Biol. Chem. 266, 10739-10742, 1991

A:Title: S-cyclophilin. New member of the cyclophilin family associated with the secr

A:Reference number: A40516; MUID:91250364

A:Accession: A40516

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-207 <CAR>

A:Cross-References: GB:M63553; NID:g212648; PIDN:AAA49064.1; PID:g212649

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase; cyclosporin A binding

F:34-196/Domain: cyclophilin homology <CYP>

Query Match

Best Local Similarity 100.0%; Score 50; DB 2; Length 207;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPMIOGGDF 9

|||||

Db 90 DPMIOGGDF 98

RESULT 6

CSHUB

peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human

N:Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000

C:Accession: A39118; A39722; A40515; S65742

R:Price, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T.

Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991

A:Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl iso

A:Reference number: A39118; MUID:91156714

A:Accession: A39118

A:Molecule type: mRNA

A:Residues: 1-208 <PRI>

A:Cross-References: GB:M60857; NID:gl81334; PIDN:AAA52150.1; PID:gl81335

R:Hazel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.

Mol. Cell. Biol. 11, 3484-3491, 1991

A:Title: An endoplasmic reticulum-specific cyclophilin.

A:Reference number: A39722; MUID:91260697

A:Accession: A39722

A:Molecule type: mRNA

A:Residues: 1-208 <HAS>

A:Cross-References: GB:M60457; NID:gl81249; PIDN:AAA35733.1; PID:gl81250

R:Spik, G.; Haendler, B.; Delmas, O.; Marillier, C.; Chamoux, M.; Maes, P.; Tartar, A.

J. Biol. Chem. 266, 10735-10738, 1991

A:Title: A novel secreted cyclophilin-like protein (SCYLP).

A:Reference number: A40515; MUID:91250363

A:Accession: A40515

A:Molecule type: mRNA

A:Residues: 'MLRLSRN', 1-208 <SPI>

A:Cross-References: GB:M63573; NID:g337998; PIDN:AAA36601.1; PID:g337999

A:Note: the authors' translation begins at an ATG codon in poor context for initiation

A:Note: parts of this sequence, including the amino end of the mature form, were conf

R:Mariller, C.; Allain, F.; Kouach, M.; Spik, G.
 Biochim. Biophys. Acta 1293, 31-38, 1996
 A:Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated form
 A:Reference number: S65742; MUID:96186273
 A:Accession: S65742
 A:Molecule type: protein
 A:Residues: 26-30;203 <MAT>
 A:Experimental source: milk
 C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence
 C:Comment: This protein binds to and is inhibited by the immunosuppressive drug cyclosporin
 C:Genetics:
 A:Gene: GDB:PP1B
 A:Cross-references: GDB:127610; OMIM:123841
 A:Map position: 15q21-15q22
 C:Function:
 C:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; glycoprotein; T-cell
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-203/Product: peptidylprolyl isomerase B #status experimental <MAT>
 F:35-197/Domain: cyclophilin homology <CYP>
 F:140/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 50; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
 |||||

Db 91 DFMIQGGDF 99

RESULT 7
 A40047
 peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin C) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
 C:Accession: A40047
 R:Friedman, J.; Weissman, I.
 Cell 66, 799-806, 1991
 A:Title: Two cytoplasmic candidates for immunophilin action are revealed by affinity for
 A:Reference number: A40047; MUID:91347379
 A:Accession: A40047
 A:Molecule type: DNA
 A:Residues: 1-212 <FRI>
 A:Cross-references: NID:g192898; PIDN:AAA37511.1; PID:g192899
 C:Comment: This protein binds the immunosuppressive drug cyclosporin A.
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding
 F:37-199/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 50; DB 2; Length 212;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
 |||||

Db 93 DFMIQGGDF 101

RESULT 8
 A56861
 peptidylprolyl isomerase (EC 5.2.1.8) CYP-S1 precursor - mouse
 N:Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
 C:Species: Mus musculus (house mouse)
 C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
 C:Accession: A56861; B39722; S21835
 R:Schumacher, A.; Schroter, H.; Muthaup, G.; Nordheim, A.
 Biochim. Biophys. Acta 1129, 13-22, 1991
 A:Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative sign
 A:Reference number: A56861; MUID:92096454

A:Accession: A56861
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-216 <SCH>
 A:Experimental source: teratocarcinoma F9 cells
 A:Note: sequence extracted from NCBI backbone (NCBI:73234, NCBI:73239)
 A:Note: parts of this sequence, including the amino end of the mature protein, were c
 R:Hasei, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
 Mol. Cell. Biol. 11, 3484-3491, 1991
 A:Title: An endoplasmic reticulum-specific cyclophilin.
 A:Reference number: A39722; MUID:91260697
 A:Accession: B39722
 A:Molecule type: mRNA
 A:Residues: 9-216 <HAS>
 A:Cross-references: GB:M60456; NID:g192864; PIDN:AAA37498.1; PID:g192865
 R:Nordheim, A.
 Submitted to the EMBL Data Library, May 1991
 A:Reference number: S21835
 A:Accession: S21835
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 9-216 <NOR>
 A:Cross-references: EMBL:X58990; NID:g53034; PIDN:CAA41736.1; PID:g53035
 C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:34-216/Product: peptidylprolyl isomerase B #status predicted <MAT>
 F:43-205/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 50; DB 2; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.0078;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
 |||||

Db 99 DFMIQGGDF 107

RESULT 9
 B53422
 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana
 N:Alternate names: cyclophilin homolog ROC4; protein F21F14.200
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 19-May-2000
 C:Accession: B53422; T47995
 R:Lippuner, V.; Chou, I.T.; Scott, S.V.; Ettinger, W.F.; Theg, S.M.; Gasser, C.S.
 J. Biol. Chem. 269, 7863-7868, 1994
 A:Title: Cloning and characterization of chloroplast and cytosolic forms of cyclophil
 A:Reference number: A53422; MUID:94179146
 A:Accession: B53422
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-260 <LIP>
 A:Cross-references: GB:L14845; NID:g405130; PIDN:AAA20048.1; PID:g405131
 R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.;
 Submitted to the Protein Sequence Database, February 2000
 A:Reference number: Z24481
 A:Accession: T47995
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <CHO>
 A:Cross-references: EMBL:AL138642
 A:Experimental source: cultivar Columbia; BAC clone F21F14
 C:Genetics:
 A:Gene: ROC4
 A:Map position: 3
 A:Introns: 18/3; 81/3; 133/1; 162/3; 181/1; 209/3
 A:Note: F21F14.200
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding
 F:94-256/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 50; DB 2; Length 260;
 Best Local Similarity 100.0%; Pred. No. 0.0096;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIQGGDF 9
 |||||

DB 150 DFMIQGGDF 158

RESULT 10

JC5314
 CDC28/cdc2-like kinase associating arginine-serine cyclophilin - human
 A:Alternate names: CARs-Cyp
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: JC5314; G02262
 R:Nestel, F.P.; Colwill, K.; Harper, S.; Pawson, T.; Anderson, S.K.
 Gene 180, 151-155, 1996
 A:Title: RS cyclophilins: Identification of an NK-Tp1-related cyclophilin.
 A:Reference number: JC5314; MUID:97128820
 A:Accession: JC5314
 A:Molecule type: mRNA
 A:Residues: 1-754 <NES>
 A:Cross-references: EMBL:U40763; NID:g1117967; PIDN:AA040347.1; PID:g1117968
 A:Experimental source: thymus
 A:Note: Submitted to the EMBL Data Library, November 1995
 C:Comment: This protein contains a cyclophilin-related domain, two 140K nuclear phosphop
 splicing by binding to splicing factors containing serine-arginine repeats protein.
 C:Genetics:
 A:Gene: GDB:CYP; CARs-CYP
 A:Cross-references: GDB:9956062
 C:Superfamily: CARs cyclophilin; cyclophilin homology
 F:7-177/Domain: cyclophilin homology <CYP>

Query Match 98.0%; Score 49; DB 1; Length 754;
 Best Local Similarity 88.9%; Pred. No. 0.052;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIQGGDF 9
 |||||

DB 71 DFMIQGGDF 79

RESULT 11

CSBY
 peptidylprolyl isomerase (EC 5.2.1.8), cytosolic - yeast (Saccharomyces cerevisiae)
 N:Alternate names: cyclophilin A; cyclosporin A-binding protein; peptidylprolyl isomeras
 C:Species: Saccharomyces cerevisiae
 C>Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 05-Nov-1999
 C:Accession: S25443; JQ0125; S57980; S29645
 R:Diemeter, K.; Tropshug, M.
 Nucleic Acids Res. 18, 373, 1990
 A:Title: Nucleotide sequence of a full-length cDNA coding for cyclophilin (peptidyl-pro
 A:Reference number: S25443; MUID:90221831
 A:Accession: S25443
 A:Molecule type: mRNA
 A:Residues: 1-162 <DIE>
 A:Cross-references: EMBL:X17505; NID:g3617; PIDN:CAA35545.1; PID:g3618
 R:Haendler, B.; Keller, R.; Hiestand, P.C.; Kocher, H.P.; Wegmann, G.; Movva, N.R.
 Gene 83, 39-46, 1989
 A:Title: Yeast cyclophilin: Isolation and characterization of the protein, cDNA and gene
 A:Reference number: JQ0125; MUID:90076969
 A:Accession: JQ0125
 A:Molecule type: DNA
 A:Residues: 1-162 <HAES>
 A:Cross-references: GB:M30513; NID:g171313; PIDN:AAA34528.1; PID:g171314
 A:Note: part of this sequence was confirmed by protein sequencing
 R:Murphy, L.; Richards, C.; Harris, D.
 submitted to the EMBL Data Library, July 1995
 A:Reference number: S57971

A:Accession: S57980
 A:Molecule type: DNA
 A:Residues: 1-162 <MUR>
 A:Cross-references: EMBL:Z50046; NID:g899393; PIDN:CAA90376.1; PID:g899403; GSPDB:GMO
 A:Experimental source: strain AB972
 R:Hasumi, H.; Nishikawa, T.
 Biochim. Biophys. Acta 1161, 161-167, 1993
 A:Title: Purification and properties of multiple molecular forms of yeast peptidyl pr
 A:Reference number: S29645; MUID:93160233
 A:Accession: S29645
 A:Molecule type: protein
 A:Residues: 'X', 3-8, 'X', 10:30-37; 75-78; 81-85; 159-162 <HAS>
 C:Genetics:
 A:Gene: SGD:CPI1; MIPS:YDR155C
 A:Cross-references: SGD:S0002562; MIPS:YDR155C
 A:Map position: 4R
 C:Function:
 A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
 A:Note: activity is one-tenth that of the mammalian protein; high binding affinity fo
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: acetylated amino end; blocked amino end; cis-trans-isomerase; cyclosporin
 F:1-162/Domain: cyclophilin homology <CYP>
 F:1-162/Product: peptidylprolyl isomerase, cytosolic #status experimental <MAT>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 96.0%; Score 48; DB 1; Length 162;
 Best Local Similarity 88.9%; Pred. No. 0.015;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIQGGDF 9
 |||||

DB 57 DFMIQGGDF 65

RESULT 12

S28020
 peptidylprolyl isomerase (EC 5.2.1.8) - Streptomyces chrysomallus
 N:Alternate names: cyclophilin A; cyclosporin A-binding protein
 C:Species: Streptomyces chrysomallus
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
 C:Accession: S28020; S25676
 R:Pahl, A.; Uehlein, M.; Bang, H.; Schlumbohm, W.; Keller, U.
 Mol. Microbiol. 6, 3551-3558, 1992
 A:Title: Streptomyces possess peptidyl-prolyl cis-trans isomerases that strongly re
 A:Reference number: S28020; MUID:93116593
 A:Accession: S28020
 A:Molecule type: DNA
 A:Residues: 1-165 <PAH>
 A:Cross-references: EMBL:Z15137; NID:g46835; PIDN:CAA78840.1; PID:g46836
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding
 F:2-165/Domain: cyclophilin homology <CYP>

Query Match 96.0%; Score 48; DB 2; Length 165;
 Best Local Similarity 88.9%; Pred. No. 0.015;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIQGGDF 9
 |||||

DB 58 DFMIQGGDF 66

RESULT 13

JT0686
 peptidylprolyl isomerase (EC 5.2.1.8) a, cytosolic - fungus (Fusarium sporotrichioides
 N:Alternate names: cyclophilin A
 C:Species: Fusarium sporotrichioides
 C>Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 19-Jan-2001
 C:Accession: JT0686; PN0166; JT0702
 R:Chow, L.P.; Ueno, Y.; Tsugita, A.
 submitted to JIPID, June 1995

A:Description: Amino acid sequence of peptidyl-prolyl isomerase a from Fusarium sporotrichi
A:Reference number: JT0686
A:Accession: JT0686
A:Molecule type: protein
A:Residues: 1-179 <CHOS>
R:Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A:Reference number: PNO160
A:Accession: PNO160
A:Molecule type: protein
A:Residues: 1-41 <FUK>
R:Chow, L.P.; Kamo, M.; Ueno, Y.; Tsugita, A.
submitted to JIPID, August 1995
A:Description: Amino acid sequence of peptidyl-prolyl isomerase a of Fusarium sporotrichi
A:Reference number: JT0702
A:Accession: JT0702
A:Molecule type: protein
A:Residues: 1-179 <CH2>
A:Comment: This enzyme catalyzes interconversion of the cis and trans imino peptide bond
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol; nucleotide binding; P-1
F:1-179/Domain: cyclophilin homology <CYP>
F:59-76/Domain: peptidylprolyl isomerase specific <PPI>
F:81-88/Region: nucleotide-binding motif A (P-loop)
F:23/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F:23/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:28/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:131/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:132/Binding site: substrate (Trp) #status predicted
F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted

Query Match 96.0%; Score 48; DB 2; Length 179;
Best Local Similarity 88.9%; Pred. No. 0.016;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
|||||
DB 70 DFMIOGGDF 78

RESULT 14
T27371
peptidylprolyl isomerase (EC 5.2.1.8) Y75B12B.2 [similarity] - Caenorhabditis elegans
N:Contains: cyclophilin
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T27371
R:White, S.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20360
A:Accession: T27371
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-171 <WIL>
A:Cross-references: EMBL:AL032663; PIDN:CAA21760.1; GSPDB:GN00023; CESP:Y75B12B.2
A:Experimental source: clone Y75B12B
C:Genetics:
A:Gene: CESP:Y75B12B.2
A:Map position: 5
A:Introns: 23/3; 107/3
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:3-171/Domain: cyclophilin homology <CYP>

Query Match 92.0%; Score 46; DB 2; Length 171;
Best Local Similarity 88.9%; Pred. No. 0.04;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
|||||
DB 70 DFMIOGGDF 78

RESULT 15
T27882
peptidylprolyl isomerase (EC 5.2.1.8) ZK520.5 [similarity] - Caenorhabditis elegans
N:Contains: cyclophilin
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T27882
R:Steward, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z20434
A:Accession: T27882
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-172 <WIL>
A:Cross-references: EMBL:Z92822; PIDN:CAB07303.1; GSPDB:GN00021; CESP:ZK520.5
A:Experimental source: clone ZK520
C:Genetics:
A:Gene: CESP:ZK520.5
A:Map position: 3
A:Introns: 23/3; 107/3
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:3-171/Domain: cyclophilin homology <CYP>

Query Match 92.0%; Score 46; DB 2; Length 172;
Best Local Similarity 88.9%; Pred. No. 0.041;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
|||||
DB 66 DFMIOGGDF 74

Search completed: January 15, 2002, 13:06:15
Job time: 226 sec

GenCore version 4.5
 Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2002, 13:05:27 ; Search time 81.32 Seconds
 (without alignments)
 8.198 Million cell updates/sec

Title: US-09-720-469-3
 Perfect score: 51
 Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_1101.*

- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	21 AAY69923	Human cyclophilin
2	51	100.0	166	21 AAG00090	Human secreted pro
3	51	100.0	211	22 AAB73302	Human cyclophilin
4	51	100.0	216	22 AAB73301	Human cyclophilin
5	51	100.0	291	21 AAB43878	Human cancer assoc
6	42	82.4	112	22 AAG75931	Human colon cancer
7	40	78.4	83	22 AAM24287	Human EST encoded
8	39	76.5	11	21 AAY69924	Human cyclophilin
9	39	76.5	207	22 AAU01197	Human cyclophilin
10	39	76.5	254	21 AAG05073	Arabidopsis thalia
11	39	76.5	259	21 AAG05072	Arabidopsis thalia

12	39	76.5	3224	19 AAW54235	Human Nup358 prote
13	38	74.5	114	22 AAB64737	Human secreted pro
14	38	74.5	315	10 AAP90099	Protein IA of N. g
15	38	74.5	315	13 AAR27483	Protein IA. Synth
16	38	74.5	326	11 AAR06037	Class IA outer mem
17	37	72.5	108	21 AAG03830	Human secreted pro
18	37	72.5	108	22 AAM20480	Peptide #6914 enco
19	37	72.5	108	22 AAG35140	Peptide #9177 enco
20	37	72.5	114	22 AAB64736	Gene 14 human secr
21	37	72.5	145	12 AAR10763	Porcine peptidyl-p
22	37	72.5	145	16 AAR72917	Porcine peptidyl p
23	37	72.5	145	16 AAR72961	Porcine peptidyl p
24	37	72.5	163	12 AAR13726	Bovine cyclophilin
25	37	72.5	164	10 AAP90431	Cyclophilin. Homo
26	37	72.5	165	19 AAW56028	Calcineurin protei
27	37	72.5	165	21 AAG03831	Human secreted pro
28	37	72.5	165	22 AAU01195	Human cyclophilin
29	36	70.6	72	22 AAB59512	Human secreted pro
30	36	70.6	141	19 AAW44367	Breast cancer-asso
31	36	70.6	141	22 AAB98719	Breast cancer-asso
32	36	70.6	276	21 AAY52295	Human isomerase ho
33	36	70.6	296	22 AAB98722	Human breast cance
34	36	70.6	301	21 AAB51902	Gene 22 human secr
35	36	70.6	301	21 AAB51903	Human secreted pro
36	36	70.6	301	22 AAB98721	Human breast cance
37	36	70.6	494	20 AAY34531	Porphyromonas ging
38	36	70.6	532	20 AAY34398	Porphyromonas ging
39	36	70.6	782	20 AAY42283	Salmonella dublin
40	35	68.6	212	21 AAY92048	A. niger peptidyl-
41	34	66.7	152	19 AAW77504	Staphylococcus aur
42	34	66.7	212	14 AAR32353	Cyclophilin C. Mu
43	34	66.7	309	16 AAR70762	Meningococcal grou
44	34	66.7	309	18 AAW21741	Neisseria meningit
45	34	66.7	313	18 AAW21744	Neisseria meningit

ALIGNMENTS

RESULT 1

AA69923

ID AAY69923 standard; peptide; 9 AA.

AC AAY69923;

XX

DT 11-APR-2000 (first entry)

XX Human cyclophilin B peptide fragment #3.

DE

XX Cyclophilin B: human; tumour antigen peptide; cytotoxic T-cell; CTL;

KW HLA antigen; diagnosis; tumour; therapy.

XX

OS Homo sapiens.

XX

PN WO9967288-A1.

XX

PD 29-DEC-1999.

XX

PF 24-JUN-1999; 99WO-JP03360.

XX

PR 25-JUN-1998; 98JP-0178449.

XX

PA (SUMU) SUMITOMO PHARM CO LTD.

PA (ITOHI) ITOH K.

XX

PI Itoh K, Gomi S;

XX

DR WPI; 2000-116932/10.

XX

PT Tumour antigen peptides derived from cyclophilin B for treatment and

XX diagnosis of tumours -

XX

PS Claim 4; Page 50; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
DB 1 gfgyknsk f 9
|||||

RESULT 2
AAG00090
ID AAG00090 standard; Protein; 166 AA.
XX
AC AAG00090;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 4171.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI: 2000-500381/45.
DR N-PSDB; AAC00096.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
XX
CC The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.
XX
SQ Sequence 166 AA;

Query Match 100.0%; Score 51; DB 21; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.076;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
DB 1 gfgyknsk f 9
|||||

RESULT 3
AAB73302
ID AAB73302 standard; protein; 211 AA.
XX
AC AAB73302;
XX
DT 22-MAY-2001 (first entry)
XX
DE Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
XX
KW Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
KW somatolactogenic function modulator; immunosuppression; short stature;
KW muscle wasting; osteoporosis; HIV infection; breast cancer;
KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia;
KW C-terminal deletion mutant; mutein.
XX
OS Homo sapiens.
XX
PN WO200113113-A1.
XX
PD 22-FEB-2001.
XX
PF 10-AUG-2000; 2000WO-US21789.
XX
PR 19-AUG-1999; 99US-0149752.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Clevenger CV, Ryczyn MA;
XX
DR WPI: 2001-211249/21.
XX
PT Novel composition for modulating somatolactogenic function, comprises
PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
PT B with somatolactogenic hormone -
XX
XX Disclosure: Page -: 21pp; English.
XX
CC The invention relates to a composition for modulating somatolactogenic
CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B
CC (particularly a CypB mutant in which residues 2-12 of the mature protein
CC are absent) or an inhibitor of the interaction of cyclophilin B with a
CC somatolactogenic hormone (e.g., prolactin, growth hormone). The invention
CC also relates to a method of identifying inhibitors of somatolactogenic
CC functions using CypB and a somatolactogenic hormone, and a method for
CC diagnosing diseases associated with abnormal somatolactogenic functions
CC by assessing CypB levels in a sample from a patient. Cyclophilin B is
CC useful for augmenting somatolactogenic function in the animal, and
CC cyclophilin B mutant or a composition comprising an inhibitor of the
CC interaction of cyclophilin B with a somatolactogenic hormone, is useful
CC for inhibiting somatolactogenic function in the animal. A composition
CC comprising cyclophilin B is useful in the treatment of immunosuppression,
CC in the treatment of short stature, muscle wasting and osteoporosis. A
CC composition comprising cyclophilin B mutant or a composition comprising
CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic
CC hormone, is useful for treating HIV infection, breast and prostate
CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
CC sequence represents a human cyclophilin B C-terminal mutant, CypB-AIAKE.
CC Note: The present sequence is not shown in the specification, but
CC is derived from the wild-type CypB sequence shown on pages 17-18.
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 51; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 0.096;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 Db 85 gfgyknskf 93

RESULT 4
 AAB73301
 ID AAB73301 standard; protein; 216 AA.

XX AC AAB73301;

XX DT 22-MAY-2001 (first entry)

XX DE Human cyclophilin B (CypB).

XX KW Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
 KW somatolactogenic function modulator; immunosuppression; short stature;
 KW muscle wasting; osteoporosis; HIV infection; breast cancer;
 KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia.

XX OS Homo sapiens.

XX PN WO200113113-A1.

XX PD 22-FEB-2001.

XX PF 10-AUG-2000; 2000WO-US21789.

XX PR 19-AUG-1999; 99US-0149752.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Clevenger CV, Ryczyn MA;

XX PR WPI; 2001-211249/21.

XX PT Novel composition for modulating somatolactogenic function, comprises
 PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
 PT B with somatolactogenic hormone -

PS Claim 1; Page 17-18; 21pp; English.

CC The invention relates to a composition for modulating somatolactogenic
 CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B
 CC (particularly a CypB mutant in which residues 2-12 of the mature protein
 CC are absent) or an inhibitor of the interaction of cyclophilin B with a
 CC somatolactogenic hormone (e.g., prolactin, growth hormone). The invention
 CC also relates to a method of identifying inhibitors of somatolactogenic
 CC functions using CypB and a somatolactogenic hormone, and a method for
 CC diagnosing diseases associated with abnormal somatolactogenic functions
 CC by assessing CypB levels in a sample from a patient. Cyclophilin B is
 CC useful for augmenting somatolactogenic function in the animal, and
 CC cyclophilin B mutant or a composition comprising an inhibitor of the
 CC interaction of cyclophilin B with a somatolactogenic hormone, is useful
 CC for inhibiting somatolactogenic function in the animal. A composition
 CC comprising cyclophilin B is useful in the treatment of immunosuppression,
 CC in the treatment of short stature, muscle wasting and osteoporosis. A
 CC composition comprising cyclophilin B mutant or a composition comprising
 CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic
 CC hormone, is useful for treating HIV infection, breast and prostate
 CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
 CC sequence represents human cyclophilin B.

XX SQ Sequence 216 AA;

Query Match 100.0%; Score 51; DB 22; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9

Db 85 gfgyknskf 93

RESULT 5
 AAB43878
 ID AAB43878 standard; Protein; 291 AA.

XX AC AAB43878;

XX DT 08-FEB-2001 (first entry)

XX DE Human cancer associated protein sequence SEQ ID NO:1323.

XX KW Human; cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;
 KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
 KW antinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
 KW dermatological; neuroprotective; thrombolytic; coagulant; vasotropic;
 KW antiprosoratic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening.

XX OS Homo sapiens.

XX PN WO200055350-A1.

XX PD 21-SEP-2000.

XX PF 08-MAR-2000; 2000WO-US05882.

XX PR 12-MAR-1999; 99US-0124270.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2000-587533/55.

XX PR N-PSDB; AAC78087.

XX PT Novel isolated nucleic acids comprising sequences encoding peptides
 XX useful for treating or diagnosing e.g. cancer -

XX PS Claim 11; Page 1974-1975; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given
 in AAB43398 to AAB4239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnery; immunomodulator;
 CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
 CC antinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 CC neotropic; vasotropic; antiprosoratic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention.

XX SQ Sequence 291 AA;

Query Match 100.0%; Score 51; DB 21; Length 291;

Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
|||||
Db 160 gfygknskf 168

RESULT 6
AAG75931
ID AAG75931 standard; Protein; 112 AA.
AC AAG75931;
XX
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:6695.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma.
XX
XX Homo sapiens.
OS
XX
PN WO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-US26524.
PF
XX
XX 29-SEP-1999; 99US-0157137.
PR
XX 03-NOV-1999; 99US-0163280.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
PI
XX
XX WPI; 2001-235357/24.
DR
XX N-PSDB; AAH35336.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
PT
XX
XX Claim 11; Page 8161-8163; 9803pp; English.
PS
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAG77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
XX Sequence 112 AA;

Query Match 82.4%; Score 42; DB 22; Length 112;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
|||||
Db 160 gfygknskf 168

RESULT 7
AAM24287
ID AAM24287 standard; Protein; 83 AA.
XX
XX
AC AAM24287;
XX
XX 12-OCT-2001 (first entry)
DT
XX
DE Human EST encoded protein SEQ ID NO: 1812.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.
XX
XX Homo sapiens.
OS
XX
PN WO200154477-A2.
XX
XX 02-AUG-2001.
PD
XX
XX 25-JAN-2001; 2001WO-US02687.
PF
XX
XX 25-JAN-2000; 2000US-0491404.
PR
XX 17-JUL-2000; 2000US-0617746.
PR
XX 03-AUG-2000; 2000US-0631451.
PR
XX 15-SEP-2000; 2000US-0663870.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
PI
XX
XX WPI; 2001-476164/51.
DR
XX N-PSDB; AAH98946.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
PT
XX
XX Claim 20; Page 1183-1184; 1275pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
XX Sequence 83 AA;

Query Match 78.4%; Score 40; DB 22; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNS 7
|||||
Db 77 gfygkns 83

RESULT 8
AAY69924
ID AAY69924 standard; peptide; 11 AA.
XX
XX
AC AAY69924;
XX
XX 11-APR-2000 (first entry)
DT
XX

DE Human cyclophilin B peptide fragment #4.
 XX Cyclophilin B: human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO967288-A1.
 XX
 PD 29-DEC-1999.
 XX
 XX 24-JUN-1999; 99WO-JP03360.
 PF
 XX 25-JUN-1998; 98JP-0178449.
 PR
 XX (SUMU) SUMITOMO PHARM CO LTD.
 PA (ITOH/) ITOH K.
 XX
 XX Itoh K, Gomi S;
 PI
 XX WPI; 2000-116932/10.
 DR
 XX Tumour antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumours -
 PT
 XX Claim 4; Page 50; 64pp; Japanese.
 PS
 XX This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours.
 XX
 XX Sequence 11 AA;
 SQ

Query Match 76.5%; Score 39; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKNSKF 9
 DB 1 gyknskf 7
 |||||
 |||||

RESULT 9
 AAU01197
 ID AAU01197 standard; Protein; 207 AA.
 XX
 AC AAU01197;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human cyclophilin D protein.
 XX
 KW Human; adenine nucleotide translocator; ANT; MTP; cyclophilin D;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200132876-A2.
 PN
 XX 10-MAY-2001.
 PD
 XX 03-NOV-2000; 2000WO-US30535.
 PF
 XX 03-NOV-1999; 99US-0434354.
 PR
 XX (MITO-) MITOKOR.
 PA
 XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelebi G, Davis RE;

XX WPI; 2001-291054/30.
 DR N-PSDB; AAS05937.
 XX
 XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 XX Disclosure; Fig 8; 186pp; English.
 PS
 XX The present sequence represents human cyclophilin D which is a
 CC mitochondrial core component. Cyclophilins interact with other
 CC mitochondrial core components e.g. adenine nucleotide translocator (ANT)
 CC proteins to regulate MPT. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. The present invention
 CC relates to a novel nucleic acid expression construct comprising a
 CC promoter operably linked to a polynucleotide encoding a mitochondrial
 CC pore component polypeptide (e.g. ANT) fused to an energy transfer
 CC molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH
 CC sequence). The novel expression construct can alter mitochondrial
 CC membrane permeability transition and/or alter the interaction between
 CC mitochondrial core components. The methods are useful for screening for
 CC agents that alter MPT and/or cell survival. These agents are useful for
 CC the prevention or treatment of diseases associated with altered
 CC mitochondrial function or dysfunctional cell survival, such as
 CC Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's
 CC disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis,
 CC stroke, hyperproliferative disorders e.g. cancer, and deafness.
 XX
 XX Sequence 207 AA;
 SQ

Query Match 76.5%; Score 39; DB 22; Length 207;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 DB 87 gfgykstf 95
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RESULT 10
 AAG05073
 ID AAG05073 standard; Protein; 254 AA.
 XX
 AC AAG05073;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 1339.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 XX EP1033405-A2.
 PN
 XX 06-SEP-2000.
 PD
 XX 25-FEB-2000; 2000EP-0301439.
 PF
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
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Query Match 76.5%; Score 39; DB 21; Length 254;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
Db 129 gfgykgstf 137
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ID AAG05072 standard; Protein; 259 AA.
XX
AC AAG05072;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1338.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Query Match 76.5%; Score 39; DB 21; Length 259;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GFGYKNSKF 9
Db 134 gfgykgstf 142
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RESULT 12
AAW54235
ID AAW54235 standard; peptide; 3224 AA.
XX
AC AAW54235;
XX
DT 10-AUG-1998 (first entry)
XX
DE Human Nup358 protein.
XX
KW Cervical cancer-associated protein; Cvc; tryptic peptide; human;
KW detection; treatment; Nup358; nucleoporin; non-chromatin protein.
XX
OS Homo sapiens.
XX
PN WO9809170-A2.
XX
PD 05-MAR-1998.
XX
PF 19-AUG-1997; 97WO-US14526.
XX
PR 30-AUG-1996; 96US-0705660.
XX
PA (MATR-) MATRITTECH INC.
XX
PI Keesee SK, Obar R, Wu Y;
XX
DR WPI: 1998-230271/20.
XX
PT Detection and therapy of cervical cancer - using specific cervical
PT cancer-associated proteins as targets for treatment or as indicators
PT for detection
XX
PS Claim 16; Page 58-65; 79pp; English.
XX
CC This protein is the human nucleoporin nup358 which is used to obtain
CC tryptic peptides which are used in a method for detecting cervical
CC cancer. The method involves detecting the presence of a cervical
CC cancer-associated protein (cvc) in a tissue or body fluid sample. The
CC cvc is characterised as having a molecular weight of 44900-69400 Daltons
CC as determined by sodium dodecyl-sulphate (SDS)-PAGE techniques and an
CC isoelectric point (pi) of 5.1-6.6 as determined by standard isoelectric
CC focusing techniques. The protein is further characterised as being a
CC non-chromatin protein which is detectable at a higher level in a human
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CC cervical cancer cell than in a normal human cervical cell, as determined
 CC by 2D-gel electrophoresis. The methods can be used for the early and
 CC rapid detection of cervical cancer, for treating cervical cancers and
 CC for monitoring the efficacy of such treatment.

XX Sequence 3224 AA;

Query Match 76.5%; Score 39; DB 19; Length 3224;
 Best Local Similarity 77.8%; Pred. No. 2.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
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 Db 3105 gfgfknslf 3113

RESULT 13

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 ID AAB64737 standard; Protein; 114 AA.

XX AAB64737;

DT 23-MAR-2001 (first entry)

DE Human secreted protein sequence encoded by gene 14 SEQ ID NO:131.

XX Human; secreted protein; diagnosis; cytostatic; antirheumatic;
 KW antiarthritic; dermatologic; cardiant; antiinflammatory; anti-ulcer;
 KW gastrointestinal; solid tumour; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; myocardial angiogenesis; Crohn's disease;
 KW ulcer.

XX Homo sapiens.

OS WO200077237-A1.

PN 21-DEC-2000.

XX 01-JUN-2000; 2000WO-US14928.

XX 11-JUN-1999; 99US-0138633.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.

XX Rosen CA, Ruben SM, Komatsoulis GA;

XX WPI; 2001-071280/08.

XX Nucleic acids encoding 49 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating diseases such as tumors,
 PT rheumatoid arthritis, psoriasis and diabetic retinopathy -

PS Disclosure; Page 500-501; 520pp; English.

XX The polynucleotide sequences given in AAF33037 to AAF33085 encode the
 CC human secreted proteins given in AAB64666 to AAB64714. AAB64715 to
 CC AAB64771 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissues
 CC and cells the genes are expressed in. Examples of activities include:
 CC cytostatic; antirheumatic; antiarthritic; dermatologic; cardiant;
 CC antiinflammatory; gastrointestinal; and anti-ulcer. The polynucleotides
 CC and polypeptides can be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate polypeptide expression.
 CC Disorders that may be treated or prevented include solid tumours,
 CC rheumatoid arthritis, psoriasis, diabetic retinopathy, myocardial
 CC angiogenesis, Crohn's disease and ulcers. The polynucleotides and their
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate
 CC the presence of similar nucleic acid sequences in samples, and therefore
 CC which patients may be in need of restorative therapy. The polypeptides

CC may also be used as antigens in the production of antibodies against the
 CC polypeptide and in assays to identify modulators (agonists and
 CC antagonists) of polypeptide expression and activity. The anti-polypeptide
 CC antibodies and antagonists may also be used to down regulate expression
 CC and activity. AAF33028 to AAF33036 and AAB64665 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 114 AA;

Query Match 74.5%; Score 38; DB 22; Length 114;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9

Db 26 gfgyksscf 34

RESULT 14

AAP90099

ID AAP90099 standard; protein; 315 AA.

XX AAP90099;

DT 01-NOV-1989 (first entry)

XX Protein IA of N. gonorrhoea strain FA19.

XX Neisseria gonorrhoea (NG); NG strain FA19; peptide sequence;
 KW Protein IA.

XX Neisseria gonorrhoea.

OS Key Location/Qualifiers

PH Region 1..18

FT /label= signal-peptide

XX WO8904873-A.

XX 01-JUN-1989.

XX 23-NOV-1988; 88WO-US04225.

XX 24-NOV-1987; 87US-0242758.

XX (UYNC) THE UNIVERSITY OF NORTH CAROLINA.

XX Carbonetti NH, Sparling PF;

XX WPI; 1989-178391/24.

XX N-PSDB; AAN90047.

XX New Neisseria gonorrhoeae Protein I gene sequences
 PT - used for detection of N. gonorrhoea infection and
 PT for producing vaccines for prevention or treatment of infection

XX Disclosure; fig 3; 70pp; English.

XX Peptide sequence of Protein IA of Neisseria gonorrhoea (NG)
 CC strain FA19. Used in prepn. of vaccines for prevention or
 CC treatment of NG infection. The region is a signal peptide.

XX Sequence 315 AA;

Query Match 74.5%; Score 38; DB 10; Length 315;
 Best Local Similarity 77.8%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9

Db 173 gfyknsgf 181

```
RESULT 15
AAR27483
ID AAR27483 standard; Protein; 315 AA.
XX
AC AAR27483;
XX
DT 08-MAR-1993 (first entry)
XX
DE Protein IA.
XX
KW Protein IB; P1B; Neisseria gonorrhoeae; P1A; outer membrane; porin;
KW hydrophobic; lipid; outer membrane; antigen; immunogen; vaccine;
KW gonorrhoea; infection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT /label= Signal_peptide
FT Protein 19..315
FT /label= Mature_protein
XX
PN W09216223-A.
XX
PD 01-OCT-1992.
XX
PF 13-MAR-1992; 92WO-US02006.
XX
PR 14-MAR-1991; 91US-0669492.
XX
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Carbonetti N, Sparling FP;
XX
WPI: 1992-348935/42.
XX
N-PSDB; AAQ29138.
XX
PT Fragments of Neisseria Gonorrhoeae protein IA or IB - used as
PT vaccines for preventing gonorrhoeal infection, and for diagnosis
XX
PS Disclosure; Fig 3; 95pp; English.
XX
CC The sequence given is encoded by the protein IA gene of Neisseria
CC gonorrhoeae. P1A is a major outer membrane proteins of N. gonorrhoeae
CC which act as a porin. Porins are believed to act in cells by
CC channelling low molecular weight substances across the hydrophobic
CC lipid outer membrane. Elucidation of the gene sequences of P1A and
CC P1B allows the production of antigenic fragments by recombinant DNA
CC techniques. These fragments can be used as immunogens in vaccine
CC compositions for the prevention of gonorrhoea, and also on immunoassays
CC for diagnosis of infection. See also AAR27484.
XX
SQ Sequence 315 AA;

Query Match 74.5%; Score 38; DB 13; Length 315;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
Db 173 gfnynsgf 181
||| ||| |

Search completed: January 15, 2002, 13:05:27
Job time: 198 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:03:58 ; Search time 37.64 Seconds
(without alignments)
5.381 Million cell updates/sec

Title: US-09-720-469-3
Perfect score: 51
Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	126	2	US-08-482-728A-10
2	51	100.0	208	1	US-08-142-897-7
3	45	88.2	161	1	US-08-145-995A-13
4	45	88.2	161	2	US-08-451-747-13
5	45	88.2	161	3	US-09-134-852-13
6	42	82.4	126	2	US-08-482-728A-11
7	40	78.4	163	1	US-08-142-897-8
8	40	78.4	164	1	US-08-145-995A-9
9	40	78.4	164	2	US-08-451-747-9
10	40	78.4	164	3	US-09-134-852-9
11	39	76.5	126	2	US-08-482-728A-12
12	39	76.5	3224	2	US-08-705-660-34
13	39	76.5	3224	3	US-08-989-045-34
14	37	72.5	126	2	US-08-482-728A-15
15	37	72.5	127	2	US-08-482-728A-9
16	37	72.5	165	1	US-08-145-995A-8
17	37	72.5	165	2	US-08-145-995A-11
18	37	72.5	165	2	US-08-451-747-8
19	37	72.5	165	2	US-08-451-747-11
20	37	72.5	165	3	US-09-134-852-8
21	37	72.5	165	3	US-09-134-852-11
22	36	70.6	141	2	US-08-658-639-14
23	36	70.6	141	4	US-08-944-604-14
24	36	70.6	276	2	US-08-989-386-3
25	36	70.6	296	4	US-08-944-604-20
26	36	70.6	301	4	US-08-944-604-18
27	34	66.7	212	1	US-08-142-897-5

28	34	66.7	309	1	US-08-096-182A-2	Sequence 2, Appli
29	34	66.7	309	1	US-08-877-109-2	Sequence 2, Appli
30	34	66.7	309	3	US-08-798-760-2	Sequence 2, Appli
31	34	66.7	309	5	PCT-US94-08327-2	Sequence 2, Appli
32	33	64.7	126	2	US-08-482-728A-16	Sequence 16, Appl
33	33	64.7	162	1	US-08-142-897-9	Sequence 9, Appli
34	33	64.7	162	1	US-08-145-995A-14	Sequence 14, Appl
35	33	64.7	162	2	US-08-451-747-14	Sequence 14, Appl
36	33	64.7	162	3	US-09-134-852-14	Sequence 14, Appl
37	32	62.7	50	1	US-08-259-672-19	Sequence 19, Appl
38	32	62.7	50	1	US-08-459-351-19	Sequence 19, Appl
39	32	62.7	50	1	US-08-460-533-19	Sequence 19, Appl
40	32	62.7	50	5	PCT-US94-06654-19	Sequence 19, Appl
41	32	62.7	148	2	US-08-886-751A-4	Sequence 4, Appli
42	32	62.7	149	1	US-08-259-672-6	Sequence 6, Appli
43	32	62.7	149	1	US-08-459-351-6	Sequence 6, Appli
44	32	62.7	149	1	US-08-460-533-6	Sequence 6, Appli
45	32	62.7	149	4	US-08-971-207-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-482-728A-10
; Sequence 10, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482.728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-482-728A-10

Query Match 100.0% Score 51; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GFGYKNSKF 9

DB 28 GFGYKSKF 36
|||||
RESULT 2
US-08-142-897-7
; Sequence 7, Application US/08142897
; Patent No. 5447852
; GENERAL INFORMATION:
; APPLICANT: Friedman, Jeffrey S.
; APPLICANT: Weissman, Irving L.
; TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tracy J. Dunn
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,897
; FILING DATE: 05-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/005,917
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,375
; FILING DATE: 05-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy D.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 5490A-92-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-897-7
Query Match 100.0%; Score 51; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFGYKSKF 9
Db 77 GFGYKSKF 85
|||||
RESULT 3
US-08-145-995A-13
; Sequence 13, Application US/08145995A
; Patent No. 5482850
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOFILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,747
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,995
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 514

ADRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-13
Query Match 88.2%; Score 45; DB 1; Length 161;
Best Local Similarity 88.9%; Pred. No. 0.27;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GFGYKSKF 9
Db 42 GFGYKSKF 50
|||||
RESULT 4
US-08-451-747-13
; Sequence 13, Application US/08451747
; Patent No. 5821107
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOFILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,747
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,995
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-451-747-13

Query Match 88.2%; Score 45; DB 2; Length 161;
Best Local Similarity 88.9%; Pred. No. 0.27;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
Db 42 GFGYKGSKF 50

RESULT 5
US-09-134-852-13
Sequence 13, Application US/09134852
Patent No. 6127148
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-134-852-13

Query Match 88.2%; Score 45; DB 3; Length 161;
Best Local Similarity 88.9%; Pred. No. 0.27;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
Db 42 GFGYKGSKF 50

RESULT 6
US-08-482-728A-11
Sequence 11, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton
& Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-11

Query Match 82.4%; Score 42; DB 2; Length 126;
Best Local Similarity 77.8%; Pred. No. 0.76;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
Db 28 GYGYKGSKF 36

RESULT 7
US-08-142-897-8
Sequence 8, Application US/08142897
Patent No. 5447852
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins

```

; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tracy J. Dunn
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142-897
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/005,917
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,375
; FILING DATE: 05-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy D.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 5490A-92-1
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-142-897-8

Query Match 78.4%; Score 40; DB 1; Length 163;
Best Local Similarity 77.8%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
DB 44 GFGYKGSF 52

RESULT 8
US-08-145-995A-9
; Sequence 9, Application US/08145995A
; Patent No. 54B2850
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tracy J. Dunn
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,995A
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 164 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-145-995A-9

Query Match 78.4%; Score 40; DB 1; Length 164;
Best Local Similarity 77.8%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
DB 45 GFGYKGSF 53

RESULT 9
US-08-451-747-9
; Sequence 9, Application US/08451747
; Patent No. 5821107
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLOGICS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,747
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,995
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-046-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 164 amino acids
; TYPE: amino acid
```

STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-451-747-9

Query Match 78.4%; Score 40; DB 2; Length 164;
 Best Local Similarity 77.8%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYKNSKF 9
 Db 45 GFGYKGSF 53

RESULT 10
 US-09-134-852-9
 ; Sequence 9, Application US/09134852
 ; Patent No. 6127148
 ; GENERAL INFORMATION:
 ; APPLICANT: CARLOW, CLOTILDE K.S.
 ; APPLICANT: PAGE, ANTONY
 ; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC COMPOUNDS
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ; ADDRESSEE: CUSHMAN
 ; STREET: 130 WATER STREET
 ; CITY: BOSTON
 ; STATE: MASSACHUSETTS
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/134,852
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/145,995
 ; FILING DATE: 29-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RESNICK, DAVID S.
 ; REGISTRATION NUMBER: 34235
 ; REFERENCE/DOCKET NUMBER: 43406
 ; TELEPHONE: (617) 523-3400
 ; TELEFAX: (617) 523-6440
 ; TELEX: 200291 STRE UR
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 164 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 US-09-134-852-9

Query Match 78.4%; Score 40; DB 3; Length 164;
 Best Local Similarity 77.8%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYKNSKF 9
 Db 45 GFGYKGSF 53

RESULT 11

US-08-482-728A-12
 ; Sequence 12, Application US/08482728A
 ; Patent No. 5968802
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Bruce
 ; APPLICANT: Fisher, Joseph
 ; APPLICANT: Payan, Donald
 ; TITLE OF INVENTION: NO. 5968802el Nuclear Cyclophilin
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton
 ; ADDRESSEE: & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,728A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Silva, Robin M.
 ; REGISTRATION NUMBER: 38,304
 ; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 126 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 US-08-482-728A-12

Query Match 76.5%; Score 39; DB 2; Length 126;
 Best Local Similarity 77.8%; Pred. No. 2.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYKNSKF 9
 Db 28 GFGYKGSF 36

RESULT 12
 US-08-705-660-34
 ; Sequence 34, Application US/08705660
 ; Patent No. 5858683
 ; GENERAL INFORMATION:
 ; APPLICANT: KEESSE, SUSAN
 ; APPLICANT: OBAR, ROBERT
 ; APPLICANT: WU, YING-JYE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 ; DETECTION OF CERVICAL CANCER
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Testa, Hurwitz & Thibault
 ; STREET: 125 High St.
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/705.660
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3224 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-705-660-34

Query Match 76.5%; Score 39; DB 2; Length 3224;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
| | | | |
Db 3105 GFGFKNSIF 3113

RESULT 13
US-08-989-045-34
; Sequence 34, Application US/08989045
; Patent No. 6027905
; GENERAL INFORMATION:
; APPLICANT: KEESE, SUSAN
; APPLICANT: OBAR, ROBERT
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; DETECTION OF CERVICAL CANCER
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,045
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GREENHALGH, DUNCAN A
; REGISTRATION NUMBER: 38,678
; REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3224 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-989-045-34

Query Match 76.5%; Score 39; DB 3; Length 3224;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
| | | | |
Db 3105 GFGFKNSIF 3113

RESULT 14
US-08-482-728A-15
; Sequence 15, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEEX: 910 277299
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-482-728A-15

Query Match 72.5%; Score 37; DB 2; Length 126;
Best Local Similarity 77.8%; Pred. No. 6.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
| | | | |
Db 28 GFGYKGSIF 36

RESULT 15
US-08-482-728A-9
; Sequence 9, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce


```

; APPLICANT: Fisher, Joseph
; APPLICANT: Pavan, Donald
; TITLE OF INVENTION: No. 5968802e1 Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-482-728A-9

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Query Match          72.5%; Score 37; DB 2; Length 127;
Best Local Similarity 77.8%; Pred. No. 6.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
Db 28 GFGYKNSCF 36

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Search completed: January 15, 2002, 13:03:59
Job time: 215 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:06:15 ; Search time 42.04 Seconds
(without alignments)
16.308 Million cell updates/sec

Title: US-09-720-469-3
Perfect score: 51
Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	183	2 S71547	peptidylprolyl iso
2	51	100.0	208	1 CSHUB	peptidylprolyl iso
3	51	100.0	216	2 A56861	peptidylprolyl iso
4	45	88.2	161	2 A45000	peptidylprolyl iso
5	42	82.4	164	2 S63995	peptidylprolyl iso
6	42	82.4	212	2 A34204	peptidylprolyl iso
7	41	80.4	207	2 A40516	peptidylprolyl iso
8	40	78.4	38	2 A56814	peptidylprolyl iso
9	40	78.4	164	1 CSHYAC	peptidylprolyl iso
10	40	78.4	164	1 CSHSA	peptidylprolyl iso
11	40	78.4	164	1 CSRTA	peptidylprolyl iso
12	40	78.4	179	2 J70686	peptidylprolyl iso
13	40	78.4	223	1 CSNCM	peptidylprolyl iso
14	39	76.5	137	2 S68767	peptidylprolyl iso
15	39	76.5	207	2 A41581	peptidylprolyl iso
16	39	76.5	3224	1 S58884	peptidylprolyl iso
17	38	74.5	308	2 S24202	Ran-binding protei
18	38	74.5	326	2 A39951	protein 1 - Neisse
19	38	74.5	330	2 PC4425	outer membrane pro
20	37	72.5	163	1 CSCK	lectin-like adhesi
21	37	72.5	163	1 CSROAB	peptidylprolyl iso
22	37	72.5	163	1 CSFGA	peptidylprolyl iso
23	37	72.5	165	1 CSHUA	peptidylprolyl iso
24	37	72.5	165	2 B38368	peptidylprolyl iso
25	36	70.6	180	2 S51497	peptidylprolyl iso
26	36	70.6	227	2 S71849	peptidylprolyl iso
27	36	70.6	301	1 S66681	peptidylprolyl iso
28	36	70.6	330	2 A70422	hypothetical prote
29	36	70.6	540	2 JC7381	DNA-directed DNA p

30 36 70.6 795 2 T21487 hypothetical prote
31 35 68.6 283 2 T31275 2-hydroxymuconate-
32 35 68.6 286 1 JC5419 probable ribose/ga
33 35 68.6 536 1 D70184 proline--tRNA liga
34 35 68.6 616 2 G86890 hypothetical prote
35 35 68.6 707 2 F72393 penicillin-binding
36 35 68.6 864 2 JH0438 genome polyprotein
37 35 68.6 3163 1 JQ1895 phosphoglycerate m
38 34.5 67.6 492 2 H81387 hypothetical prote
39 34 66.7 121 2 D82882 peptidylprolyl iso
40 34 66.7 165 2 S28020 peptidylprolyl iso
41 34 66.7 212 2 A40047 outer membrane pro
42 34 66.7 293 2 S25509 outer membrane pro
43 34 66.7 294 2 S25508 outer membrane pro
44 34 66.7 295 2 S25507 outer membrane pro
45 34 66.7 295 2 S25506 outer membrane pro

ALIGNMENTS

RESULT 1

S71547
peptidylprolyl isomerase (EC 5.2.1.8) B. 20.3K - rat
N:Alternate names: cyclophilin B; PPIASE
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C:Accession: S71547
R:Ruecknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaefer, M.; Fischer, G.
submitted to the Protein Sequence Database, November 1996
A:Reference number: S71547
A:Accession: S71547
A:Molecule type: protein
A:Residues: 1-183 <RUE>
A:Experimental source: liver
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <MAT>
F:10-172/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 51; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
|||||
DB 52 GFGYKNSKF 60

RESULT 2

CSHUB
peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human
N:Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000
C:Accession: A39118; A39722; A40515; S65742
R:Price, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T.
Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991
A:Title: Human cyclophilin B; a second cyclophilin gene encodes a peptidyl-prolyl iso
A:Reference number: A39118; MUID:91156714
A:Accession: A39118
A:Molecule type: mRNA
A:Residues: 1-208 <PRI>
A:Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335
R:Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
Mol. Cell. Biol. 11, 3484-3491, 1991
A:Title: An endoplasmic reticulum-specific cyclophilin.
A:Reference number: A39722; MUID:91260697
A:Accession: A39722
A:Molecule type: mRNA
A:Residues: 1-208 <HAS>
A:Cross-references: GB:M60457; NID:g181249; PIDN:AAA35733.1; PID:g181250

R:Spik, G.; Haendler, B.; Delmas, O.; Mariller, C.; Chamoux, M.; Maes, P.; Tartar, A.; J. Biol. Chem. 266, 10735-10738, 1991
 A:Title: A novel secreted cyclophilin-like protein (SCVLP).
 A:Reference number: A40515; MUID:91250363
 A:Accession: A40515
 A:Molecule type: mRNA
 A:Residues: 'MRLSRN', 1-208 <SPI>
 A:Cross-references: GB:M63573; NID:g337998; PIDN:AAA36601.1; PID:g337999
 A:Note: the authors' translation begins at an ATG codon in poor context for initiation
 R:Mariller, C.; Allain, F.; Kouach, M.; Spik, G. Biochim. Biophys. Acta 1293, 31-38, 1996
 A:Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated form
 A:Reference number: S65742; MUID:96186273
 A:Accession: S65742
 A:Molecule type: protein
 A:Residues: 26-30; 203 <MAR>
 A:Experimental source: milk
 C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence
 C:Comment: This protein binds to and is inhibited by the immunosuppressive drug cyclosporin
 C:Genetics:
 A:Gene: GDB:PPIB
 A:Cross-references: GDB:127610; OMIM:123841
 A:Map position: 15q21-15q22
 C:Function:
 A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
 C:Superfamily: peptidylprolyl isomerase; cyclophilin A binding; glycoprotein; T-cell
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; glycoprotein; T-cell
 F:1-25/Domain: signal sequence status predicted <SIG>
 F:26-203/Product: peptidylprolyl isomerase B #status experimental <MAT>
 F:35-197/Domain: cyclophilin homology <CYP>
 F:140/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 51; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 DB 77 GFGYKNSKF 85
 |||||

RESULT 3
 A56861
 peptidylprolyl isomerase (EC 5.2.1.8) Cyp-S1 precursor - mouse
 N:Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
 C:Accession: A56861; B39722; S21835
 R:Schumacher, A.; Schroter, H.; Multhaup, G.; Nordheim, A. Biochim. Biophys. Acta 1129, 13-22, 1991
 A:Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative signal
 A:Reference number: A56861; MUID:92096454
 A:Accession: A56861
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-216 <SCH>
 A:Experimental source: teratocarcinoma F9 cells
 A:Note: sequence extracted from NCBI backbone (NCBIN:73234, NCBIP:73239)
 A:Note: parts of this sequence, including the amino end of the mature protein, were confirmed
 R:Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G. Mol. Cell. Biol. 11, 3484-3491, 1991
 A:Title: An endoplasmic reticulum-specific cyclophilin.
 A:Reference number: A39722; MUID:91260697
 A:Accession: B39722
 A:Molecule type: mRNA
 A:Residues: 9-216 <HAS>
 A:Cross-references: GB:M60456; NID:g192864; PIDN:AAA37498.1; PID:g192865
 R:Nordheim, A. submitted to the EMBL Data Library, May 1991
 A:Reference number: S21835
 A:Accession: S21835

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 9-216 <NOR>
 A:Cross-references: EMBL:X58990; NID:g53034; PIDN:CAA1736.1; PID:g53035
 C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:34-216/Product: peptidylprolyl isomerase B #status predicted <MAT>
 F:43-205/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 51; DB 2; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 DB 85 GFGYKNSKF 93
 |||||

RESULT 4
 A45000
 peptidylprolyl isomerase (EC 5.2.1.8) [similarity] - tapeworm (Echinococcus granulosus)
 N:Contains: cyclophilin
 C:Species: Echinococcus granulosus
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 08-Sep-2000
 C:Accession: A45000
 R:Lightowers, M.W.; Haralambous, A.; Rickard, M.D. Mol. Biochem. Parasitol. 36, 287-289, 1989
 A:Title: Amino acid sequence homology between cyclophilin and a cDNA-cloned antigen o
 A:Reference number: A45000; MUID:90014983
 A:Accession: A45000
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-161
 A:Cross-references: GB:J04664; NID:g158843; PIDN:AAA29058.1; PID:g158844
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase
 F:1-161/Domain: cyclophilin homology <CYP>

Query Match 88.2%; Score 45; DB 2; Length 161;
 Best Local Similarity 88.9%; Pred. No. 0.26;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 DB 42 GFGYKNSKF 50
 |||||

RESULT 5
 S63995
 peptidylprolyl isomerase (EC 5.2.1.8) - German cockroach
 N:Alternate names: cyclophilin
 C:Species: Blattella germanica (German cockroach)
 C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
 C:Accession: S63995
 R:Martinez-Gonzalez, J.; Hegardt, F.G. Eur. J. Biochem. 234, 284-292, 1995
 A:Title: Characterization of a cDNA encoding a cytosolic peptidylprolyl cis-trans-iso
 A:Reference number: S63995; MUID:96096751
 A:Accession: S63995
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-164 <MAR>
 A:Cross-references: EMBL:X87418; NID:g1235942; PIDN:CAA60869.1; PID:g1772496
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase
 F:3-164/Domain: cyclophilin homology <CYP>

Query Match 82.4%; Score 42; DB 2; Length 164;

Best Local Similarity 77.8%; Pred. No. 0.98;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
||||| I:I
Db 45 GFGYKGSRF 53

RESULT 6
A54204
peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human
N:Alternate names: cyclophilin C
C:Species: Homo sapiens (man)
C:Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A54204
R:Schneider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesnel
Biochemistry 33, 8218-8224, 1994
A:Title: Human cyclophilin C: primary structure, tissue distribution, and determination
A:Reference number: A54204; MUID:94304830
A:Accession: A54204
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-212 <SCH>
A:Cross-references: GB:S71018; NID:g547303; PIDN:AAB31350.1; PID:g547304
A:Experimental source: kidney
A:Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBI:P:149388)
C:Genetics:
A:Gene: GDB:PPIC
A:Cross-references: GDB:136196; OMIM:123842
A:Map position: 15q21-15q22
C:Superfamily: peptidylprolyl isomerase: cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F:37-199/Domain: cyclophilin homology <CYP>

Query Match 82.4%; Score 42; DB 2; Length 212;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
||||| I:I
Db 79 GFGYKGSKF 87

RESULT 7
A40516
peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
C:Accession: A40516
R:Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.
J. Biol. Chem. 266, 10739-10742, 1991
A:Title: S-cyclophilin. New member of the cyclophilin family associated with the secretory
A:Reference number: A40516; MUID:91250364
A:Accession: A40516
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-207 <CAR>
A:Cross-references: GB:M63553; NID:g212648; PIDN:AAA49064.1; PID:g212649
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F:34-196/Domain: cyclophilin homology <CYP>

Query Match 80.4%; Score 41; DB 2; Length 207;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
||||| I:I
Db 76 GFGYKGSKF 84

RESULT 8
A56814
peptidylprolyl isomerase (EC 5.2.1.8) [similarity] - mouse (fragments)
N:Alternate names: cyclophilin homolog SIP24
C:Species: Mus musculus (house mouse)
C:Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 02-Sep-2000
C:Accession: A56814
R:Davis, T.R.; Tabatabai, L.; Bruns, K.; Hamilton, R.T.; Nilsen-Hamilton, M.
Biochim. Biophys. Acta 1095, 145-152, 1991
A:Title: Basic fibroblast growth factor induces 3T3 fibroblasts to synthesize and sec
A:Reference number: A56814; MUID:92031730
A:Accession: A56814
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-38 <DAV>
A:Experimental source: BALB/c 3T3 cells
A:Note: sequence modified after extraction from NCBI backbone
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase

Query Match 78.4%; Score 40; DB 2; Length 38;
Best Local Similarity 77.8%; Pred. No. 0.54;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
||||| I:I
Db 13 GFGYKGSF 21

RESULT 9
CSHYAC
peptidylprolyl isomerase (EC 5.2.1.8) A - Chinese hamster
N:Alternate names: cyclophilin A; cyclosporin A-binding protein A
C:Species: Crictetus griseus (Chinese hamster)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: S07597
R:Bergsma, D.J.; Sylvester, D.
Nucleic Acids Res. 18, 200, 1990
A:Title: A Chinese hamster ovary cyclophilin cDNA sequence.
A:Reference number: S07597; MUID:90174932
A:Accession: S07597
A:Molecule type: mRNA
A:Residues: 1-164 <BER>
A:Cross-references: EMBL:X17105; NID:g49495; PIDN:CAA34961.1; PID:g49496
C:Function:
A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding; T-cell
F:3-164/Domain: cyclophilin homology <CYP>

Query Match 78.4%; Score 40; DB 1; Length 164;
Best Local Similarity 77.8%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
||||| I:I
Db 45 GFGYKGSF 53

RESULT 10
CSWSA
peptidylprolyl isomerase (EC 5.2.1.8) A - mouse
N:Alternate names: cyclophilin A; cyclosporin A-binding protein A
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: S10327; S66416; S40742
R:Hasel, K.W.; Sutcliffe, J.G.
Nucleic Acids Res. 18, 4019, 1990
A:Title: Nucleotide sequence of a cDNA coding for mouse cyclophilin.
A:Reference number: S10327; MUID:90326555
A:Accession: S10327

A:Molecule type: mRNA
A:Residues: 1-164 <HAS>
A:Cross-references: GB:X52803; NID:g50620; PIDN:CAA36989.1; PID:g50621
R:Krummel, U.; Bang, R.; Schmidtschen, R.; Brune, K.; Bang, H.
FEBS Lett. 371, 47-51, 1995
A:Title: Cyclophilin-A is a zinc-dependent DNA binding protein in macrophages.
A:Reference number: S66416; MUID:95394146
A:Accession: S66416
A:Molecule type: protein
A:Residues: 2-21 <RRU>
A:Experimental source: nuclear cyclophilin of H4-7 cells
C:Genetics:
A:Gene: CypA
C:Function:
A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding; DNA binding; macrophage; T-cell;
F:3-164/Domain: cyclophilin homology <CYP>

Query Match 78.4%; Score 40; DB 1; Length 164;
Best Local Similarity 77.8%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
||||| I I
Db 45 GFGYKGSSSF 53

RESULT 11
CSRTA
peptidylprolyl isomerase (EC 5.2.1.8) A - rat
N:Alternate names: 13.3K protein [misidentification]; cyclophilin A; cyclosporin A-binding protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 04-Feb-2000
C:Accession: A29819; A60036; A15632; A36859
R:Danielson, P.E.; Forss-Petter, S.; Brow, M.A.; Calavetta, L.; Douglass, J.; Milner, R.
DNA 7, 261-267, 1988
A:Title: pIB15: A cDNA clone of the rat mRNA encoding cyclophilin.
A:Reference number: A29819; MUID:88283345
A:Accession: A29819
A:Molecule type: mRNA
A:Residues: 1-164 <DBAN>
A:Cross-references: GB:M19533; NID:g203701; PIDN:AAA41009.1; PID:g203702
R:Lad, R.P.; Smith, M.A.; Hilt, D.C.
Brain Res. Mol. Brain Res. 9, 235-244, 1991
A:Title: Molecular cloning and regional distribution of rat brain cyclophilin.
A:Reference number: A60036; MUID:91232390
A:Accession: A60036
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-164 <LAD>
A:Experimental source: brain
R:Theodor, L.; Peleg, D.; Meyuhas, O.
Biochim. Biophys. Acta 826, 137-146, 1985
A:Title: P31, a mammalian housekeeping protein encoded by a multigene family containing
A:Reference number: A15632; MUID:86026347
A:Accession: A15632
A:Molecule type: mRNA
A:Residues: 100-148; MARPARRSPPTVGNPNFDRAPVPSNH', 'SFCSGGEHPHICQYDVISALTEVLWVP', 'YF
A:Cross-references: EMBL:M25637
A:Note: this sequence was corrected by A58859
R:Meyuhas, O.
submitted to GenBank, December 1991
A:Reference number: A58859
A:Contents: erratum
A:Accession: A58859
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-164 <MEY>
A:Cross-references: EMBL:M25637; NID:g951424; PIDN:AA859719.1; PID:g951425
A:Note: the submission to GenBank in entry RAYP31 is acknowledged as an unpublished error
C:Comment: This protein belongs to a class of highly conserved proteins, abundant in th

C:Function:
A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding; T-cell
F:3-164/Domain: cyclophilin homology <CYP>

Query Match 78.4%; Score 40; DB 1; Length 164;
Best Local Similarity 77.8%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
||||| I I
Db 45 GFGYKGSSSF 53

RESULT 12
JT0686
peptidylprolyl isomerase (EC 5.2.1.8) a, cytosolic - fungus (Fusarium sporotrichioides)
N:Alternate names: cyclophilin A
C:Species: Fusarium sporotrichioides
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 19-Jan-2001
C:Accession: JT0686; PNO166; JT0702
R:Chow, L.P.; Ueno, Y.; Tsugita, A.
submitted to JIPID, June 1995
A:Description: Amino acid sequence of peptidyl-prolyl isomerase a from Fusarium sporotrichioides
A:Reference number: JT0686
A:Accession: JT0686
A:Molecule type: protein
A:Residues: 1-179 <CHO>
R:Fukaya, N.; Chow, L.P.; Sugiyama, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A:Reference number: PNO160
A:Accession: PNO166
A:Molecule type: protein
A:Residues: 1-41 <FKU>
R:Chow, L.P.; Kamo, M.; Ueno, Y.; Tsugita, A.
submitted to JIPID, August 1995
A:Description: Amino acid sequence of peptidyl-prolyl isomerase a of Fusarium sporotrichioides
A:Reference number: JT0702
A:Accession: JT0702
A:Molecule type: protein
A:Residues: 1-179 <CH2>
C:Comment: This enzyme catalyzes interconversion of the cis and trans imino peptide b
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol; nucleotide binding;
F:1-179/Domain: cyclophilin homology <CYP>
F:59-76/Domain: peptidylprolyl isomerase specific <PPI>
F:81-88/Region: nucleotide-binding motif A (P-loop)
F:23,172/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predi
F:23/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:28/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:131/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:132/Binding site: substrate (trp) #status predicted
F:172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pre

Query Match 78.4%; Score 40; DB 2; Length 179;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
||||| I I
Db 56 GFGYKGSSSF 64

RESULT 13
CSNCM
peptidylprolyl isomerase (EC 5.2.1.8) precursor, mitochondrial - Neurospora crassa
N:Alternate names: cyclophilin B; cyclosporin A-binding protein B
N:Contains: peptidylprolyl isomerase (EC 5.2.1.8), cytosolic (cyclophilin A, cyclosporin
C:Species: Neurospora crassa

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C:Accession: B30809; A30809; S07585
 R:Tropschug, M.; Nicholson, D.W.; Hartl, F.U.; Koehler, H.; Pfanner, N.; Wachter, E.; Ne
 J. Biol. Chem. 263, 14433-14440, 1998
 A:Title: Cyclosporin A-binding protein (cyclophilin) of Neurospora crassa. One gene code
 A:Reference number: A92671; MUID:89008293
 A:Accession: B30809
 A:Molecule type: mRNA
 A:Residues: 1-223 <TR0>
 A:Cross-references: GB:J03963; NID:gl168805; PIDN:AAA33584.1; PID:gl168806
 A:Accession: A30809
 A:Molecule type: mRNA
 A:Residues: 44-223 <TR2>
 A:Cross-references: GB:J03963
 R:Tropschug, M.
 Nucleic Acids Res. 18, 190, 1990
 A:Title: Nucleotide sequence of the gene coding for cyclophilin/peptidyl-prolyl cis-tran
 A:Reference number: S07585; MUID:90174923
 A:Accession: S07585
 A:Molecule type: DNA
 A:Residues: 1-223 <TR02>
 A:Cross-references: EMBL:X17692; NID:g2998; PIDN:CAA35681.1; PID:g295926
 C:Comment: The mature cytosolic and mitochondrial forms are identical in sequence, altho
 for the mitochondrial form begins at an upstream initiator available from alternative sp
 inal residue.
 C:Function:
 A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: alternative initiators; alternative splicing; cis-trans-isomerase; cyclospor
 F:1-180/Product: peptidylprolyl isomerase mitochondrial form precursor #status predicted
 F:1-36/Domain: transit peptide (mitochondrion) #status predicted <TNP>
 F:37-44/Domain: propeptide #status predicted <PRO>
 F:44-223/Domain: cyclophilin homology <CYP>
 F:44-180/Product: peptidylprolyl isomerase cytosolic form precursor #status predicted <
 F:45-180/Product: peptidylprolyl isomerase, cytosolic #status experimental <CMAT>
 F:45-180/Product: peptidylprolyl isomerase, mitochondrial #status experimental <MMAT>

Query Match 78.4%; Score 40; DB 1; Length 223;
 Best Local Similarity 77.8%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYKNSKF 9
 |||||
 Db 100 GFGYKGSF 108

RESULT 14

S68767
 peptidylprolyl isomerase (EC 5.2.1.8) - rat (fragments)
 N:Alternate names: cyclophilin
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 11-Jun-1999
 C:Accession: S68767
 R:Rianveer, A.; Virji, S.; Andreeva, L.; Totty, N.F.; Hsuan, J.J.; Ward, J.M.; Crompton,
 Eur. J. Biochem. 238, 166-172, 1996
 A:Title: Involvement of cyclophilin D in the activation of a mitochondrial pore by Ca(2+
 A:Reference number: S68767; MUID:96248435
 A:Accession: S68767
 A:Molecule type: protein
 A:Residues: 1-13;14-23;29:30-60;61-77;78-100;101-114;115-137 <TAN>
 A:Experimental source: liver
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; mitochondrion

Query Match 76.5%; Score 39; DB 2; Length 137;
 Best Local Similarity 77.8%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYKNSKF 9
 |||||
 Db 41 GFGYKGSF 49

RESULT 15

A41581
 peptidylprolyl isomerase (EC 5.2.1.8) 3 precursor - human
 N:Contains: cyclophilin
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 02-Sep-2000
 C:Accession: A41581
 R:Bergsma, D.J.; Eder, C.; Gross, M.; Kersten, H.; Sylvestre, D.; Appelbaum, E.; Cusi
 T. W.P.; Bossard, M.J.; Brandt, M.; Levy, M.A.
 J. Biol. Chem. 266, 23204-23214, 1991
 A:Title: The cyclophilin multigene family of peptidyl-prolyl isomerases. Characteriza
 A:Reference number: A41581; MUID:92078192
 A:Accession: A41581
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-207 <BER>
 A:Cross-references: GB:M80254; NID:gl181273; PIDN:AAA58434.1; PID:gl181274
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; mitochondrion
 F:45-206/Domain: cyclophilin homology <CYP>

Query Match 76.5%; Score 39; DB 2; Length 207;
 Best Local Similarity 77.8%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYKNSKF 9
 |||||
 Db 87 GFGYKGSF 95

Search completed: January 15, 2002, 13:06:15
 Job time: 226 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: January 15, 2002, 13:14:58 ; Search time 24.88 Seconds
(Without alignments)
13.263 Million cell updates/sec

Title: US-09-720-469-3
Perfect score: 51
Sequence: 1 GFCYKNSKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	51	100.0	208	1 CYPB_HUMAN	P23284 homo sapien
2	51	100.0	208	1 CYPB_MOUSE	P24369 mus musculus
3	51	100.0	208	1 CYPB_RAT	P24368 rattus norv
4	46	90.2	208	1 CYPB_BOVIN	P80311 bos taurus
5	45	88.2	161	1 CYPH_ECHGR	P14088 echinococu
6	42	82.4	164	1 CYPH_BLAG	P54985 blattella g
7	42	82.4	212	1 CYPB_HUMAN	P45877 gallus gall
8	41	80.4	207	1 CYPB_CHICK	P24367 gallus gall
9	40	78.4	163	1 CYPH_CRILO	P14851 cricetus
10	40	78.4	163	1 CYPB_MOUSE	P17742 mus musculus
11	40	78.4	163	1 CYPH_RAT	P10111 rattus norv
12	40	78.4	223	1 CYPH_NEUCR	P10255 neurospora
13	39	76.5	206	1 CYPB_RAT	P29117 rattus norv
14	39	76.5	207	1 CYPB_HUMAN	P30405 homo sapien
15	39	76.5	3224	1 RBP2_HUMAN	P49792 homo sapien
16	38	74.5	326	1 OMA_NEIGO	P05430 neisseria g
17	37	72.5	162	1 CYPH_CANAL	P22011 candida alb
18	37	72.5	163	1 CYPH_BOVIN	P04374 bos taurus
19	37	72.5	164	1 CYPH_HUMAN	P05092 homo sapien
20	37	72.5	165	1 CYPH_DROME	P25007 drosophila
21	36	70.6	298	1 CYPB_MOUSE	P95093 mus musculus
22	36	70.6	301	1 CYPE_HUMAN	P95093 mus musculus
23	36	70.6	658	1 ADAS_CAVPO	P97275 cavia porce
24	36	70.6	658	1 ADAS_HUMAN	P00116 homo sapien
25	35	68.6	749	1 CATA_LEGPN	P09489 legionella
26	35	68.6	853	1 FBPA_HAEIN	P31776 h penicilli
27	35	68.6	3163	1 POLG_TUMVQ	Q02597 t genome po
28	35	68.6	3164	1 POLG_TUMVJ	P89509 t genome po
29	34	66.7	165	1 PPI_STRCH	Q06118 streptomyc
30	34	66.7	212	1 CYPC_MOUSE	P30412 mus musculus
31	34	66.7	310	1 API_CHICK	P18870 gallus gall
32	34	66.7	314	1 API_SERCA	P54864 serinus can
33	34	66.7	329	1 OMB_NEIMA	P57042 neisseria m

34	34	66.7	331	1 OMB1_NEIMB	P30687 neisseria m
35	34	66.7	331	1 OMB2_NEIMB	P30688 neisseria m
36	34	66.7	331	1 OMB3_NEIMB	P30689 neisseria m
37	34	66.7	331	1 OMB4_NEIMB	P30690 neisseria m
38	34	66.7	396	1 YD18_YEAST	Q12185 saccharomyc
39	34	66.7	638	1 KRAF_XENLA	P09560 xenopus lae
40	34	66.7	1085	1 RBP2_BOVIN	P48820 bos taurus
41	33	64.7	161	1 CYPH_YEAST	P14832 saccharomyc
42	33	64.7	185	1 SSRG_HUMAN	Q9unl2 homo sapien
43	33	64.7	185	1 SSRG_RAT	Q90113 rattus norv
44	33	64.7	363	1 OMPC_KLEPN	Q48473 klebsiella
45	33	64.7	454	1 SCRB_STRMU	P13522 streptococc

ALIGNMENTS

RESULT 1
CYPB_HUMAN
ID CYPB_HUMAN STANDARD: PRT: 208 AA.
AC P23284;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
GN PPIB OR CYPB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-40.
RX MEDLINE=91156714; PubMed=2000394;
RA Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,
RA Walsh C.T.;
RT *Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-
prolyl isomerase with a signal sequence.*;
RL Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91250363; PubMed=2040592;
RA Spik G., Haendler B., Delmas O., Mariller C., Chamoux M., Maes P.,
RA Tartar A., Montreuil J., Stedman K., Kocher H.P., Keller R.,
RA Hiestand P.C., Movva N.R.;
RT *A novel secreted cyclophilin-like protein (SCYLP)*;
RL J. Biol. Chem. 266:10735-10738(1991).
RN [3]
RP SEQUENCE OF 2-208 FROM N.A.
RX MEDLINE=91260697; PubMed=1710767;
RA Hasel K.W., Glass J.K., Godbout M., Sutcliffe J.G.;
RT *An endoplasmic reticulum-specific cyclophilin.*;
RL Mol. Cell. Biol. 11:3484-3491(1991).
RN [4]
RP SEQUENCE OF 64-76 AND 151-157.
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT *Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.*;
RL Electrophoresis 13:960-969(1992).
RN [5]
RP SUBCELLULAR LOCATION.
RX MEDLINE=92112948; PubMed=1530944;
RA Arber S., Krause K.-H., Caroni P.;
RT *S-cyclophilin is retained intracellularly via a unique COOH-terminal
sequence and colocalizes with the calcium storage protein
calreticulin.*;
RL J. Cell Biol. 116:113-125(1992).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=94255495; PubMed=8197205;
RA Mikol V., Kallen J., Walkinshaw M.D.;

RT *X-ray structure of a cyclophilin B/cyclosporin complex: comparison
 RT domain.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).
 RL -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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DR EMBL; M60857; AAA52150.1; -;
 DR EMBL; M63573; AAA36601.1; ALT_INIT.
 DR EMBL; M60457; AAA35733.1; -;
 DR PIR; A39118; CSHUB.
 DR PIR; A40515; A40515.
 DR PDB; 1CYN; 29-JAN-96.
 DR Aarhus/Ghent-2DPAGE; 117; NEPHGE.
 DR MIM; 123841; -;
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family; 3D-structure.
 FT SIGNAL 1 25
 FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
 FT SITE 139 208 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 208 AA; 22742 MW; A814481B7EBD4579 CRC64;

Query Match 100.0%; Score 51; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 |||||
 DB 77 GFGYKNSKF 85

RESULT 2
 CYPB_MOUSE
 ID CYPB_MOUSE STANDARD; PRT; 208 AA.
 AC P24369;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-SI).
 GN PP1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91260697; PubMed=1710767;
 RA Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
 RT "An endoplasmic reticulum-specific cyclophilin.";
 RL Mol. Cell. Biol. 11:3484-3491(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RX MEDLINE=92096454; PubMed=1756174;

RA Schumacher A., Schroeter H., Multhaup G., Nordheim A.;
 RT "Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a
 RT putative signal sequence expressed in differentiating F9 cells.";
 RL Biochim. Biophys. Acta 1129:13-22(1991).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC

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DR EMBL; M60456; AAA37498.1; -;
 DR EMBL; X58990; CAA41736.1; -;
 DR PIR; B39722; B39722.
 DR PIR; S21835; S21835.
 DR HSP; P23284; ICYN.
 DR MGD; MGI:97750; Pp1b.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family.
 FT SIGNAL 1 25 BY SIMILARITY..
 FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
 FT SITE 199 208 PREVENT SECRETION FROM ER
 FT (BY SIMILARITY).
 SQ SEQUENCE 208 AA; 22713 MW; 4B8DF5AE40BAD3A7 CRC64;

Query Match 100.0%; Score 51; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 |||||
 DB 77 GFGYKNSKF 85

RESULT 3
 CYPB_RAT
 ID CYPB_RAT STANDARD; PRT; 208 AA.
 AC P24368;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-SI).
 GN PP1B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90300692; PubMed=2194056;
 RI Iwai N., Inagami T.;
 RT "Molecular cloning of a complementary DNA to rat cyclophilin-like
 RT protein mRNA.";
 RL Kidney Int. 37:1460-1465(1990).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RX MEDLINE=92112948; PubMed=1530944;
 RA Arber S., Krause K.-H., Caroni P.;

RT "S-cyclophilin is retained intracellularly via a unique COOH-terminal
RT sequence and colocalizes with the calcium storage protein
RT calreticulin."

RL J. Cell Biol. 116:113-125(1992).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
DR HSP; P23284; ICYN.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER
FT (BY SIMILARITY).
SQ SEQUENCE 208 AA; 23025 MW; 76D12AC3427FEF32 CRC64;

Query Match 100.0%; Score 51; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFGYKNSKF 9
|||||
DB 77 GFGYKNSKF 85

RESULT 4
CYPB_BOVIN

ID CYPB_BOVIN STANDARD; PRT; 208 AA.
AC P80311;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
GN PP1B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Carrello A., Mark P.J., House A.K., Ratajczak T.;
RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 26-71.
RC TISSUE=Brain;
RX MEDLINE=94283623; PubMed=8013656;
RA Galat A., Bouet F.;
RT "Cyclophilin-B is an abundant protein whose conformation is similar
RT to cyclophilin-A";
RL FEBS Lett. 347:31-36(1994).
RN [3]
RP SEQUENCE OF 26-45.
RX MEDLINE=94280416; PubMed=8010972;
RA Bose S., Muecke M., Freedman R.B.;
RT "The characterization of a cyclophilin-type peptidyl prolyl
RT cis-trans-isomerase from the endoplasmic-reticulum lumen";
RL Biochem. J. 300:871-875(1994).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.

CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----

DR EMBL; D14073; BAA03158.1; -
DR HSP; P23284; ICYN.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER.
FT CONFLICT 30 30 K -> G (IN REF. 3).
SQ SEQUENCE 208 AA; 22701 MW; 0097C88289AF6276 CRC64;

Query Match 90.2%; Score 46; DB 1; Length 208;
Best Local Similarity 88.9%; Pred. No. 0.16;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFGYKNSKF 9
|||||
DB 77 GFGYKNSKF 85

RESULT 5
CYPH_ECHGR

ID CYPH_ECHGR STANDARD; PRT; 161 AA.
AC P14088;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (FRAGMENT).
OS Echinococcus granulosis.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
OC Rhabditophora; Eulecithophora; Revertospermata; Mediofusata;
OC Neodermata; Cestoda; Eucestoda; Cyclophyllidae; Taeniidae;
OX Echinococcus.
RN NCBI_TaxID=6210;
RP SEQUENCE FROM N.A.
RX MEDLINE=90014983; PubMed=2677720;
RA Lightowlers M.W., Haralambous A., Rickard M.D.;
RT "Amino acid sequence homology between cyclophilin and a cDNA-cloned
RT antigen of Echinococcus granulosis";
RL Mol. Biochem. Parasitol. 36:287-290(1989).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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CC -----
DR EMBL: J04564; AAA29058.1; -.
DR PIR: A45000; A45000.
DR HSP: P05092; 3CYS.
DR InterPro: IPR002130; CSA_PP1ase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PROSITE: PS00170; CSA_PP1ase_1; 1.
DR PROSITE: PS00072; CSA_PP1ase_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Multigene family.
FT NON_TER 1
SQ SEQUENCE 161 AA; 17223 MW; 72661E2F4FEF466F CRC64;

Query Match      88.2%; Score 45; DB 1; Length 161;
Best Local Similarity 88.9%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFQYKNSKF 9
DB 42 GFQYKGSKF 50

RESULT 6
CYPH_BLAGE
ID CYPH_BLAGE STANDARD; PRT; 164 AA.
AC P54985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
GN CYPA.
OS Blattella germanica (German cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthoptera; Dictyoptera; Blattaria;
OC Blaberidae; Blattellidae; Blattellinae; Blattella.
OX NCBI_TaxID=6973;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96096751; PubMed=8529654;
RA Martinez-Gonzalez J., Hegardt F.G.;
RT *Characterization of a cDNA encoding a cytosolic peptidylprolyl cis-
RT trans-isomerase from Blattella germanica.*;
RL Eur. J. Biochem. 234:284-292(1995).
CC 1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC 1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC 1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC 1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC 1- TISSUE SPECIFICITY: UBQUITOUS.
CC 1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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CC -----
DR EMBL: X87418; AAG60869.1; -.
DR HSP: P05092; 1AWY.
DR InterPro: IPR002130; CSA_PP1ase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PP1ase_1; 1.
DR PROSITE: PS00072; CSA_PP1ase_2; 1.
KW Cyclosporin; Isomerase; Rotamase.
SQ SEQUENCE 164 AA; 17935 MW; A5E25B574DFDC99 CRC64;

Query Match      82.4%; Score 42; DB 1; Length 164;

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Best Local Similarity 77.8%; Pred. No. 0.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFQYKNSKF 9
DB 45 GFQYKGSRF 53

RESULT 7
CYPC_HUMAN
ID CYPC_HUMAN STANDARD; PRT; 212 AA.
AC P45877;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN C).
GN PPIC OR CYPC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94304830; PubMed=8031755;
RA Schneider H., Charara N., Schmitz R., Wehrli S., Mikol V.,
RA Zurini M.G., Quesniaux V.F., Movva N.R.;
RT "Human cyclophilin C: primary structure, tissue distribution, and
RT determination of binding specificity for cyclosporins.";
RL Biochemistry 33:8218-8224(1994).
CC 1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC 1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC 1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
CC 1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC 1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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CC -----
DR EMBL: S71018; AAB31350.1; -.
DR HSP: P05092; 2RMC.
DR MIM: 123842; -.
DR InterPro: IPR002130; CSA_PP1ase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PP1ase_1; 1.
DR PROSITE: PS00072; CSA_PP1ase_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Multigene family.
SQ SEQUENCE 212 AA; 22763 MW; 6F3DB547A7AE581B CRC64;

Query Match      82.4%; Score 42; DB 1; Length 212;
Best Local Similarity 77.8%; Pred. No. 0.88;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFQYKNSKF 9
DB 79 GFQYKGSKF 87

RESULT 8
CYPB_CHICK
ID CYPB_CHICK STANDARD; PRT; 207 AA.
AC P24367;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 36, Last annotation update)

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DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91250364; PubMed=2040593;
 RA Caroni P., Rothenfluh A., McGlynn E., Schneider C.;
 RT "S-cyclophilin. New member of the cyclophilin family associated with
 the secretory pathway.";
 RL J. Biol. Chem. 266:10739-10742(1991).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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 CC -----
 CC EMBL: M63553; AAA49064.1; -;
 DR PIR: A40516; A40516.
 DR HSP: P23284; LCYN.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS00072; CSA_PPIASE_2; 1.
 DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 207 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
 FT SITE 198 207 PREVENT SECRETION FROM ER
 FT (BY SIMILARITY).
 SQ SEQUENCE 207 AA; 22413 MW; D9C0C2E528E25B59 CRC64;

 Query Match 80.4%; Score 41; DB 1; Length 207;
 Best Local Similarity 77.8%; Pred. No. 1.3;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 GFGYKNSKF 9
 Db 76 GFGKGSKF 84
 |||||
 RESULT 9
 ID CYPH_CRIL0 STANDARD; PRT; 163 AA.
 AC P14851;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
 DE (CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN).
 GN PPIA.
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90174932; PubMed=2408007;

RA Bergsma D.J., Sylvester D.;
 RT "A Chinese hamster ovary cyclophilin cDNA sequence.";
 RL Nucleic Acids Res. 18:200-200(1990).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
 CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X17105; CAA34961.1; -;
 DR PIR: S07597; CSHYAC.
 DR HSP: P05092; 3CYS.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS00072; CSA_PPIASE_2; 1.
 DR Cyclosporin; Isomerase; Rotamase; Multigene family.
 KW INIT_MET 0
 FT INIT_MET 0
 SQ SEQUENCE 163 AA; 17768 MW; 02D44F71B8F87A1A CRC64;

 Query Match 78.4%; Score 40; DB 1; Length 163;
 Best Local Similarity 77.8%; Pred. No. 1.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GFGYKNSKF 9
 Db 44 GFGYKGSF 52
 |||||
 RESULT 10
 ID CYPH_MOUSE STANDARD; PRT; 163 AA.
 AC P17742;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
 DE (CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (SP18).
 GN PPIA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=90326555; PubMed=2197604;
 RA Hasel K.W., Sutcliffe J.G.;
 RT "Nucleotide sequence of a cDNA coding for mouse cyclophilin.";
 RL Nucleic Acids Res. 18:4019-4019(1990).
 RN [2]
 RP SEQUENCE OF 1-19; 21-27 AND 76-84.
 RC TISSUE=Macrophage;
 RX MEDLINE=92228816; PubMed=1565646;
 RA Sherry B., Varlett N., Strupp A., Cerami A.;
 RT "Identification of cyclophilin as a proinflammatory secretory product
 of lipopolysaccharide-activated macrophages.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3511-3515(1992).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.

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CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----
CC EMBL; X52803; CAA36989.1; -.
CC PIR; S10327; CSMSA.
CC HSP; P05092; 3CYS.
CC DR SWISS-2DPAGE; P17742; MOUSE.
CC MGD; MGI:97749; Ppia.
CC InterPro: IPR002130; CSA_PPIase.
CC Pfam: PF00160; pro_isomerase; 1.
CC PRINTS; PR00153; CSAPPISMRASE.
CC PROSITE; PS00170; CSA_PPIASE_1; 1.
CC PROSITE; PS0072; CSA_PPIASE_2; 1.
CC Cyclosporin; Isomerase; Rotamase; Multigene family.
KW CYCLOSPORIN; Isomerase; Rotamase; Multigene family.
FT INIT_MET 0
FT CONFLICT 17 19 GRV -> TXP (IN REF. 2).
SQ SEQUENCE 163 AA; 17840 MW; AC724D4DBBF4840 CRC64;

Query Match 78.4%; Score 40; DB 1; Length 163;
Best Local Similarity 77.8%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
DB 44 GFGYKGSSF 52

      ||||| |
      ||||| |

RESULT 11
CYPH_RAT
ID CYPH_RAT STANDARD; PRT; 163 AA.
AC P1011; P18303;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (P31).
GN PPIA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=88283345; PubMed=3293952;
RA Danielson P.E., Forss-Petter S., Brow M.A., Calavetta L.,
RA Douglas J., Milner R.J., Sutcliffe J.G.;
RT "p1815: a cDNA clone of the rat mRNA encoding cyclophilin.";
RL DNA 7:261-267(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91232390; PubMed=1851525;
RA Lad R.P., Smith M.A., Hilt D.C.;
RT "Molecular cloning and regional distribution of rat brain
RT cyclophilin.";
RL Brain Res. Mol. Brain Res. 9:239-244(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SABRA;
RX MEDLINE=86026347; PubMed=2996604;
RA Theodor L., Peleg D., Meyuhas O.;

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RT *p31, a mammalian housekeeping protein encoded by a multigene family
RT containing a high proportion of pseudogenes.";
RL Biochim. Biophys. Acta 826:137-146(1985).
RN [4]
RP SEQUENCE OF 1-28.
RC TISSUE=Liver;
RX MEDLINE=92287042; PubMed=1599421;
RA Connern C.P., Halesrap A.P.;
RT "Purification and N-terminal sequencing of peptidyl-prolyl cis-trans-
RT isomerase from rat liver mitochondrial matrix reveals the existence
RT of a distinct mitochondrial cyclophilin.";
RL Biochem. J. 284:381-385(1992).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
CC FRAMESHIFTS.
CC -----
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CC -----
CC EMBL; M19533; AAA1009.1; -.
CC EMBL; M25637; AAB59719.1; -.
CC PIR; A15632; CSRT31.
CC PIR; A29819; CSRTA.
CC HSP; P05092; 3CYS.
CC InterPro: IPR002130; CSA_PPIase.
CC Pfam; PF00160; pro_isomerase; 1.
CC PRINTS; PR00153; CSAPPISMRASE.
CC PROSITE; PS00170; CSA_PPIASE_1; 1.
CC PROSITE; PS0072; CSA_PPIASE_2; 1.
CC Cyclosporin; Isomerase; Rotamase; Multigene family.
KW CYCLOSPORIN; Isomerase; Rotamase; Multigene family.
FT INIT_MET 0
FT CONFLICT 17 19 GRV -> TXP (IN REF. 2).
SQ SEQUENCE 163 AA; 17743 MW; DD16D1C980474414 CRC64;

Query Match 78.4%; Score 40; DB 1; Length 163;
Best Local Similarity 77.8%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
DB 44 GFGYKGSSF 52

      ||||| |
      ||||| |

RESULT 12
CYPH_NEUCR
ID CYPH_NEUCR STANDARD; PRT; 223 AA.
AC P10255;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (CPH).
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=74-OR23-1A;
RX MEDLINE=89008293; PubMed=2971658;
RA Tropischug M., Nicholson D.W., Hartl F.-U., Kohler H., Pfanner N.,
RA Wachter E., Neupert W.;

```

RT "Cyclosporin A-binding protein (cyclophilin) of Neurospora crassa.
 RL One gene codes for both the cytosolic and mitochondrial forms."
 RN J. Biol. Chem. 263:14433-14440(1988).
 RP [2]
 RX SEQUENCE FROM N.A.
 RM MEDLINE=90174923; PubMed=2137907;
 RA Trotschug M.;
 RT "Nucleotide sequence of the gene coding for cyclophilin/peptidyl-
 RL prolyl cis-trans isomerase of Neurospora crassa."
 RL Nucleic Acids Res. 18:190-190(1990).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
 CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL AND CYTOPLASMIC.
 CC -!- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS
 CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC
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 CC
 DR EMBL: J03963; AAA33584.1;
 DR EMBL: X17692; CAA33581.1;
 DR EMBL: X17692; CAA33582.1;
 DR PIR: A30809; CSNCC.
 DR PIR: B30809; CSNCC.
 DR HSP: P05092; 3CYS.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Mitochondrion; Transit peptide;
 KW Alternative Initiation.
 FT TRANSIT 1 44 MITOCHONDRION.
 FT CHAIN 45 223 PPIASE, MITOCHONDRIAL ISOFORM.
 FT CHAIN 44 223 PPIASE, CYTOSOLIC ISOFORM.
 FT INIT_MET 44 44 FOR CYTOSOLIC ISOFORM.
 SQ SEQUENCE 223 AA; 24064 MW; D494AB77F9768AE0 CRC64;
 Query Match 78.4%; Score 40; DB 1; Length 223;
 Best Local Similarity 77.8%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GFGYKNSKF 9
 Db 100 GFGYKGSF 108
 RESULT 13
 ID CYPM_RAT STANDARD; PRT; 206 AA.
 AC P29117;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR
 DE (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
 GN PPIF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-WISTAR; TISSUE=Skeletal muscle;
 RA Price N.T., Woodfield K.Y., Halestrap A.P.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 30-58.
 RX TISSUE=Liver;
 RM MEDLINE=92287042; PubMed=1599421;
 RA Conner C.P., Halestrap A.P.;
 RT "Purification and N-terminal sequencing of peptidyl-prolyl cis-trans-
 RL isomerase from rat liver mitochondrial matrix reveals the existence
 RT of a distinct mitochondrial cyclophilin."
 RL Biochem. J. 284:381-385(1992).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC
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 CC
 DR EMBL: U68544; AA08453.1;
 DR PIR: S23122; S23122.
 DR HSP: P05092; 3CYS.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;
 KW Transit peptide.
 FT TRANSIT 1 29 MITOCHONDRION.
 FT CHAIN 30 206 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
 FT VARIANT 30 39 MISSING (IN A MINOR FORM).
 FT VARIANT 31 31 S -> R.
 FT CONFLICT 30 30 C -> A (IN REF. 2).
 SQ SEQUENCE 206 AA; 21810 MW; 69048482631B9FAD CRC64;
 Query Match 76.5%; Score 39; DB 1; Length 206;
 Best Local Similarity 77.8%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GFGYKNSKF 9
 Db 86 GFGYKGSF 94
 RESULT 14
 ID CYPM_HUMAN STANDARD; PRT; 207 AA.
 AC P30405;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR
 DE (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
 GN PPIF OR CYP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92078182; PubMed=1744118;
 RA Bergsma D.J., Eder C., Gross M., Kersten H., Sylvester D.,
 RA Appelbaum E., Cusimano D., Livi G.P., McLaughlin M.M., Kasvan K.,
 RA Porter T.G., Silverman C., Dunnington D., Hand A., Prichett W.P.,

RA Bossard M.J., Brandt M., Levy M.A.;
RT "The cyclophilin multigene family of peptidyl-prolyl isomerases.
RT Characterization of three separate human isoforms.";
RL J. Biol. Chem. 266:23204-23214(1991).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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CC EMBL: M80254; AAA58434.1; -
DR PIR: A41581; A41581.
DR HSP: P05092; 3CYS.
DR MIM: 604486; -
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; isomerase; Rotamase; Multigene family; Mitochondrion;
FT Transit peptide.
FT TRANSIT 1 29 MITOCHONDRION (POTENTIAL).
FT CHAIN 30 207 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
SQ SEQUENCE 207 AA; 22040 MW; D7C76F1D4049F16A CRC64;

Query Match 76.5%; Score 39; DB 1; Length 207;
Best Local Similarity 77.8%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
| | | | | | | |
DB 87 GFGYKGSTF 95

RESULT 15
RBP2_HUMAN STANDARD; PRT; 3224 AA.
ID RBP2_HUMAN
AC P49792; Q15280;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PAN-BINDING PROTEIN 2 (RANBP2) (NUCLEAR PORE COMPLEX PROTEIN NUP358)
DE (NUCLEOPORIN NUP358) (358 KDA NUCLEOPORIN) (P270).
GN RANBP2 OR NUP358.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95294031; PubMed=7775481;
RA Wu J., Matunis M.J., Kraemer D., Blobel G., Coutavas E.;
RT "Nup358, a cytoplasmically exposed nucleoporin with peptide repeats,
RT Ran-GTP binding sites, zinc fingers, a cyclophilin A homologous
RT domain, and a leucine-rich region";
RL J. Biol. Chem. 270:14209-14213(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95327194; PubMed=7603572;
RA Yokoyama N., Hayashi M., Seki T., Nishii K., Hayashida T.,
RA Kuma K.I., Miyata T., Fukui M., Nishimoto T., Pante N., Aebi U.;
RT "A giant nucleopore protein that binds Ran/TC4";
RL Nature 376:184-188(1995).

RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.96 ANGSTROMS) OF 1171-1304.
RX MEDLINE=99176415; PubMed=10078529;
RA Vetter I.R., Nowak C., Nishimoto T., Kuhlmann J., Wittlinghofer A.;
RT "Structure of a Ran-binding domain complexed with Ran bound to a GTP
RT analogue: Implications for nuclear transport.";
RL Nature 398:39-46(1999).
CC -1- FUNCTION: INVOLVED IN TRANSPORT FACTOR (RAN-GTP, KARYOPHERIN)-
CC MEDIATED PROTEIN IMPORT VIA THE F-G REPEAT-CONTAINING DOMAIN WHICH
CC ACTS AS A DOCKING SITE FOR SUBSTRATES. COULD ALSO HAVE ISOMERASE
CC OR CHAPERONE ACTIVITY AND MAY BIND RNA OR DNA. COMPONENT OF THE
CC NUCLEAR EXPORT PATHWAY. SPECIFIC DOCKING SITE FOR THE NUCLEAR
CC EXPORT FACTOR EXPORTIN-1.
CC -1- SUBUNIT: FORMS A TIGHT COMPLEX IN ASSOCIATION WITH RANBP1 AND THE
CC URBQUITIN-CONJUGATING ENZYME E2 (UBC9) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX, CYTOPLASMIC FILAMENTS.
CC -1- DOMAIN: CONTAINS MANY X-X-F-G AND X-F-X-F-G REPEATS.
CC -1- SIMILARITY: CONTAINS 4 RANBP1-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 8 RANBP-TYPE ZINC FINGERS.
CC -1- SIMILARITY: CONTAINS A CYCLOPHILIN-LIKE PPIASE DOMAIN.
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CC EMBL: L41840; AAC41758.1; -
DR EMBL: D42063; BAA07662.1; -
DR PDB: 1RRP; 18-MAY-99.
DR MIM: 601181; -
DR InterPro: IPR002130; CSA_PPIase.
DR InterPro: IPR000697; RanBp1_WASP.
DR InterPro: IPR000156; Ran_Bp1.
DR InterPro: IPR001440; TPR.
DR InterPro: IPR001876; Znf-RanBP.
DR Pfam: PF00160; pro_isomerase; 1.
DR Pfam: PF00638; Ran_Bp1; 4.
DR Pfam: PF00515; TPR; 1.
DR Pfam: PF00641; zf-RanBP; 8.
DR PRINTS: PR00153; CSAPPISMASE.
DR SMART: SM00160; RanBD; 4.
DR SMART: SM00547; Znf_RBZ; 8.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
KW Nuclear protein; Transport; Repeat; Zinc-finger; Isomerase; Rotamase;
KW 3D-structure.
FT DOMAIN 1172 1301 RANBP1-LIKE 1.
FT ZN_FING 1356 1375 RANBP-TYPE 1.
FT ZN_FING 1419 1439 RANBP-TYPE 2.
FT ZN_FING 1483 1503 RANBP-TYPE 3.
FT ZN_FING 1547 1567 RANBP-TYPE 4.
FT ZN_FING 1610 1630 RANBP-TYPE 5.
FT ZN_FING 1669 1689 RANBP-TYPE 6.
FT ZN_FING 1728 1748 RANBP-TYPE 7.
FT ZN_FING 1785 1805 RANBP-TYPE 8.
FT DOMAIN 2013 2142 RANBP1-LIKE 2.
FT DOMAIN 2310 2439 RANBP1-LIKE 3.
FT DOMAIN 2912 3040 RANBP1-LIKE 4.
FT DOMAIN 3063 3224 PPIASE, CYCLOPHILIN-TYPE.
FT CONFLICT 777 777 R -> H (IN REF. 2).
FT CONFLICT 784 784 R -> K (IN REF. 2).
SQ SEQUENCE 3224 AA; 358214 MW; 54E78412C96A3C63 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 3224;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GFGYKNSKF 9
| | | | | | | |

Db 3105 GFGKNSIF 3113

Search completed: January 15, 2002, 13:14:59
Job time: 655 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:16:25 ; Search time 78.85 Seconds
(without alignments)
16.696 Million cell updates/sec

Title: US-09-720-469-3
Perfect score: 51
Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	208	11	O88541
2	51	100.0	216	4	Q9BVK5
3	51	100.0	216	11	O9DCY1
4	48	94.1	203	3	O01490
5	42	82.4	104	13	Q98UE5
6	41	80.4	164	5	O9XZ25
7	40	78.4	17	11	Q9QVH8
8	40	78.4	39	11	Q9RL37
9	40	78.4	70	11	Q9ERB9
10	40	78.4	143	5	Q25093
11	40	78.4	164	11	Q9CWJ5
12	40	78.4	167	11	Q9CZK9
13	40	78.4	173	10	Q9FW22
14	39	76.5	78	5	Q9U8K2
15	39	76.5	147	5	Q9N717
16	39	76.5	158	6	Q9N0U4
17	39	76.5	164	5	P91791
18	39	76.5	177	5	O02614
19	39	76.5	206	11	Q99KR7

20	39	76.5	259	10	Q9FY98	Q9fy98 arabidopsis
21	39	76.5	259	10	Q9ASS6	Q9ass6 arabidopsis
22	39	76.5	3053	11	Q9ERU9	Q9eru9 mus musculus
23	38	74.5	162	5	O00845	O00845 paramécieum
24	38	74.5	187	5	Q9U9R3	Q9u9r3 leishmania
25	38	74.5	303	2	Q9RF90	Q9rf90 neisseria g
26	38	74.5	303	2	Q9RF89	Q9rf89 neisseria g
27	38	74.5	303	2	Q9RF88	Q9rf88 neisseria g
28	38	74.5	303	2	Q9RF87	Q9rf87 neisseria g
29	38	74.5	303	2	Q9RF86	Q9rf86 neisseria g
30	38	74.5	303	2	Q9RF85	Q9rf85 neisseria g
31	38	74.5	303	2	Q9RF84	Q9rf84 neisseria g
32	38	74.5	303	2	Q9RF83	Q9rf83 neisseria g
33	38	74.5	303	2	Q9RF82	Q9rf82 neisseria g
34	38	74.5	303	2	Q9R2R5	Q9r2r5 neisseria g
35	38	74.5	303	2	Q9EZ31	Q9ez31 neisseria g
36	38	74.5	304	2	Q9EZ33	Q9ez33 neisseria g
37	38	74.5	304	2	Q9EZ32	Q9ez32 neisseria g
38	38	74.5	308	2	O51011	O51011 neisseria g
39	38	74.5	326	2	O51945	O51945 neisseria g
40	38	74.5	326	2	O51946	O51946 neisseria g
41	38	74.5	326	2	O51948	O51948 neisseria g
42	38	74.5	326	2	Q924K8	Q924k8 neisseria g
43	38	74.5	326	2	Q924K1	Q924k1 neisseria g
44	38	74.5	326	2	O51944	O51944 neisseria g
45	38	74.5	327	2	O52693	O52693 neisseria g

ALIGNMENTS

RESULT 1

O88541
ID O88541
AC O88541; PRELIMINARY; PRT; 208 AA.
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYCLOPHILIN B (EC 5.2.1.8).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR-KYOTO; TISSUE=KIDNEY;
RA Kainer D.B., Doris P.A.;
RT "Cyclophilin B";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; AF071225; AAC25590.1; -.
DR HSSP; P23284; ICYN.
DR InterPro; IPR002130; CSA_PPPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPPIase_1; 1.
DR PROSITE; PS50072; CSA_PPPIase_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 208 AA; 22802 MW; 02408DFA7157218C CRC64;

Query Match 100.0%; Score 51; DB 11; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.083;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GFGYKNSKF 9

Db 77 GFGYKNSKF 85

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RESULT 2
Q9BVK5 ID Q9BVK5 PRELIMINARY; PRT: 216 AA.
DR 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN, AND MELANOMA;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001125; AA01125.1; -.
KW Isomerase.
SQ SEQUENCE. 216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;

Query Match 100.0%; Score 51; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
DB 85 GFGYKNSKF 93

RESULT 3
Q9DCY1 ID Q9DCY1 PRELIMINARY; PRT: 216 AA.
DR 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE PEPTIDYLPROLYL ISOMERASE B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.*";
RL Nature 409:685-690(2001).
DR EMBL; AK002357; BAB22036.1; -.
DR MGD; MGI:97750; Prib.
DR InterPro; IPR002130; CSA_ppriase.
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DR pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS50072; CSA_PPIASE_2; 1.
SQ SEQUENCE 216 AA; 23713 MW; CE9DAD1544AE72FE CRC64;

Query Match 100.0%; Score 51; DB 11; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
DB 85 GFGYKNSKF 93

RESULT 4
Q01490 ID Q01490 PRELIMINARY; PRT: 203 AA.
AC Q01490;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (CYCLOPHILIN B) (ROTAMASE).
DN CYPB.
OS Orpinomyces sp. PC-2.
OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
OC Neocallimastacaceae; Orpinomyces.
OX NCBI_TaxID=50059;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
RX MEDLINE=95223986; PubMed=7708690;
RA Chen H., Li X.-L., Ljungdahl L.G.;
RT "A cyclophilin from the polycentric anaerobic rumen fungus Orpinomyces
sp. strain PC-2 is highly homologous to vertebrate cyclophilin B.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:2587-2591(1995).
CC -|- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -|- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -|- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC EMBL; U17900; AA004195.1; -.
DR HSGP; P23284; ICYN.
DR Mendel; 20786; Unkp:1040;20786.
DR InterPro; IPR002130; CSA_PPIase.
DR pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS50072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase; Signal; Cyclosporin; Endoplasmic reticulum.
FT SIGNAL 1 22
FT CHAIN 23 203 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT BINDING 147 147 CSA (POTENTIAL).
FT SITE 200 203 PREVENT SECRETION FROM ER (BY
FT SIMILARITY).
SQ SEQUENCE 203 AA; 21969 MW; A5748C94305B8BE0 CRC64;

Query Match 94.1%; Score 48; DB 3; Length 203;
Best Local Similarity 88.9%; Pred. No. 0.29;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
DB 71 GFGYKNSKF 79

RESULT 5
Q98UE5 ID Q98UE5 PRELIMINARY; PRT: 104 AA.
AC Q98UE5;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
```

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE_B (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Amano T., Yoshizato K.;
 RT "Isolation of genes involved in intestinal remodeling during anuran
 metamorphosis.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF170328; AAK11503.1;
 KW Isomerase.
 FT NON_TER 104 104
 SQ SEQUENCE 104 AA; 11350 MW; 8F6AD1CD1C2FB3E2 CRC64;

Query Match 82.4%; Score 42; DB 13; Length 104;
 Best Local Similarity 77.8%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 I:|||||
 Db 77 GYGKGSKF 85

RESULT 6
 ID Q9XZ25 PRELIMINARY; PRT; 164 AA.
 AC Q9XZ25;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CYCLOPHILIN A (EC 5.2.1.8).
 GN CYPA.
 OS Lumbricus rubellus (Humus earthworm).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 OC Lumbricina; Lumbricidae; Lumbricus.
 OX NCBI_TaxID=35632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sturzenbaum S.R., Morgan A.J., Kille P.;
 RT "Isolated from earthworms exposed to Cd-supplemented artificial
 soil.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 TRANS ISOMERASE FAMILY.
 DR EMBL; AJ238310; CAB41016.1;
 DR HSSP; P05092; 1CWL.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSA_PPIASMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 FT NON_TER 164 AA; 17599 MW; B30D22D660966AE7 CRC64;

Query Match 80.4%; Score 41; DB 5; Length 164;
 Best Local Similarity 77.8%; Pred. No. 4.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 I:|||||
 Db 45 GFGKGSKF 53

RESULT 7
 ID Q9QVH8 PRELIMINARY; PRT; 17 AA.
 AC Q9QVH8;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE SUPERINDUCIBLE PROTEIN 24, SIP24-CYCLOPHILIN HOMOLOG, PEAK A.
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92031730; PubMed=1932134;
 RA Davis T.R., Tabatabai L., Bruns K., Hamilton R.T., Nilsen-Hamilton M.;
 RT "Basic fibroblast growth factor induces 3T3 fibroblasts to synthesize
 and secrete a cyclophilin-like protein and beta 2-microglobulin.";
 RL Biochim. Biophys. Acta 1095:145-152(1991).
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 SQ SEQUENCE 17 AA; 1785 MW; 11276657FEB240D9 CRC64;

Query Match 78.4%; Score 40; DB 11; Length 17;
 Best Local Similarity 77.8%; Pred. No. 0.65;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 I:|||||
 Db 8 GFGYKGSF 16

RESULT 8
 ID Q9R137 PRELIMINARY; PRT; 39 AA.
 AC Q9R137;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CYCLOPHILIN A (FRAGMENT).
 GN PPIA OR CYPA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Ola;
 RA Colgan J.D., Asmal M., Luban J.;
 RT "Haploinsufficient growth defects, increased Th2 cytokine production
 and cyclosporine resistance in mice lacking CYPA.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF171073; AAD50996.1;
 DR HSSP; P05092; 2CPL.
 DR MGD; MGI:97749; Ppia.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4324 MW; CB53F70E1092889C CRC64;

Query Match 78.4%; Score 40; DB 11; Length 39;
 Best Local Similarity 77.8%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
 I:|||||
 Db 21 GFGYKGSF 29

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RESULT 9
Q9R9B9 ID Q9R9B9 PRELIMINARY; PRT; 70 AA.
AC Q9R9B9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLOPHILIN (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Kirigiti P., Bai Y., Li X., Machida C.A.;
RT "Mesocricetus auratus cyclophilin partial cDNA coding sequence.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC -!- FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC -!- PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC -!- TRANS ISOMERASE FAMILY.
EMBL: AY004869; AAG00259.1; -.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
FT NON_TER 1
FT NON_TER 70
FT NON_TER 70
SQ SEQUENCE 70 AA; 7841 MW; 472374C1287ACEC9 CRC64;

Query Match 78.4%; Score 40; DB 11; Length 70;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
Db 24 GFGYKGSF 32

RESULT 10
Q25093 ID Q25093 PRELIMINARY; PRT; 143 AA.
AC Q25093;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLOPHILIN-A (EC 5.2.1.8).
GN HYP.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE FROM N.A.
RA Korneev S., Blackshaw S.E., Kaiser K., Davies J.A.;
RT "cDNA libraries from identified neurons";
RL Proc. R. Soc. Lond., B, Biol. Sci. 263:57-62(1996).
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC -!- FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC -!- PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC -!- TRANS ISOMERASE FAMILY.
EMBL: U36797; AAB01531.1; -.
DR HSP; P05092; 2CPL.

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DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 143 AA; 15398 MW; 64FFD82018480A6B CRC64;

Query Match 78.4%; Score 40; DB 5; Length 143;
Best Local Similarity 77.8%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9
Db 24 GFGYKGSF 32

RESULT 11
Q9CWJ5 ID Q9CWJ5 PRELIMINARY; PRT; 164 AA.
AC Q9CWJ5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PEPTIDYLPROLYL ISOMERASE A.
GN PPIA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyogawa H., Kondo S., Yamane I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann N., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC -!- FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC -!- PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC -!- TRANS ISOMERASE FAMILY.
EMBL: AK010649; BAB27089.1; -.
DR MGD; MGI:97749; Ppia.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 164 AA; 17984 MW; DIC8D3E825F0392F CRC64;

```

Query Match

78.4%; Score 40; DB 11; Length 164;

Best Local Similarity 77.8%; Pred. No. 6.7;
Matches 7; Conservative: 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYKNSKF 9
||||| 1
Db 45 GFGYKGSF 53

RESULT 12

ID Q9CZK9 PRELIMINARY; PRT; 167 AA.
AC Q9CZK9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PEPTIDYLPROLYL ISOMERASE A.
GN PPIA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRIO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; AK012491; BAB28276.1; -.
DR MGD; MGI:97749; Ppia.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE.1; 1.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 167 AA; 18314 MW; 399BC62857BDA9EB CRC64;

Query Match 78.4%; Score 40; DB 11; Length 167;
Best Local Similarity 77.8%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYKNSKF 9
||||| 1
Db 48 GFGYKGSF 56

RESULT 13

Q9FW22

ID Q9FW22 PRELIMINARY; PRT; 173 AA.
AC Q9FW22;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO ARABIDOPSIS THALIANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
DE (P34791) (FRAGMENT).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
RA Chen C.-S., Shaw J.-F.;
RA "Oryza sativa PAC P0036D10 genomics sequence, complete sequence.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC073405; AAG03106.1; -.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
FT NON_TER 173 173
SQ SEQUENCE 173 AA; 19158 MW; 28ADE80F4625EB9 CRC64;

Query Match 78.4%; Score 40; DB 10; Length 173;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GFGYKNSKF 9
||||| 1
Db 78 GFGYKGSF 86

RESULT 14

ID Q9U8K2 PRELIMINARY; PRT; 78 AA.
AC Q9U8K2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (FRAGMENT).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ANTENNAE;
RA Renucci M., Tirard A., Matarazzo V., Belaich A., Clement J.L.;
RT "Isolation of a cDNA sequence encoding a peptidyl-prolyl cis-trans
RT isomerase from Periplaneta americana antennae.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; AF041412; AAD56049.1; -.
DR HSP; P05092; 2CPL.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE.1; 1.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 8341 MW; DB73CC5CF97334B0 CRC64;

Query Match 76.5%; Score 39; DB 5; Length 78;
 Best Local Similarity 77.8%; Pred. NO. 4.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GFGYKNSKF 9
 |||||
 DB 2 GFGYKGSTF 10

RESULT 15

Q9N717 PRELIMINARY; PRT; 147 AA.
 AC Q9N717;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE PROBABLE CYCLOPHILIN (FRAGMENT).
 GN LM12.959.
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Murphy L.; Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
 RA Oliver K.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 CC FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 CC TRANS ISOMERASE FAMILY.
 DR EMBL; AL390114; CAB98318.1; ..
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 FT NON_TER 1
 FT NON_TER 147
 SQ SEQUENCE 147 AA; 15620 MW; 9074B7BC8980B4EA CRC64;

Query Match 76.5%; Score 39; DB 5; Length 147;
 Best Local Similarity 77.8%; Pred. NO. 9.1;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GFGYKNSKF 9
 |||||
 DB 30 GFGYANSPP 38

Search completed: January 15, 2002, 13:16:25
 Job time: 656 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:05:27 ; Search time 81.32 Seconds
(without alignments)
10.020 Million cell updates/sec

Title: US-09-720-469-4
Perfect score: 60
Sequence: 1 GYKNSKPHRVI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	11	21 AAY69924	Human cyclophilin
2	60	100.0	166	21 AAG00090	Human secreted pro
3	60	100.0	211	22 AAB73302	Human cyclophilin
4	60	100.0	216	22 AAB73301	Human cyclophilin
5	60	100.0	291	21 AAB43878	Human cancer assoc
6	48	80.0	171	22 AAB49141	Caenorhabditis ele
7	48	80.0	180	19 AAB80784	D. discoideum cycl
8	48	80.0	183	21 AAB56701	Human prostate can
9	48	80.0	207	22 AAB01197	Human cyclophilin
10	48	80.0	252	21 AAG16463	Arabidopsis thalia
11	48	80.0	254	21 AAG05073	Arabidopsis thalia

12	48	80.0	254	21 AAG16462	Arabidopsis thalia
13	48	80.0	259	21 AAG05072	Arabidopsis thalia
14	48	80.0	260	21 AAG16461	Arabidopsis thalia
15	48	80.0	3224	19 AAW54235	Human Nup358 prote
16	47	78.3	129	21 AAG54741	Arabidopsis thalia
17	47	78.3	191	21 AAG15070	Arabidopsis thalia
18	47	78.3	192	21 AAG48166	Arabidopsis thalia
19	47	78.3	201	21 AAG29380	Arabidopsis thalia
20	47	78.3	205	21 AAG15069	Arabidopsis thalia
21	47	78.3	206	21 AAG48165	Arabidopsis thalia
22	47	78.3	218	21 AAG29379	Arabidopsis thalia
23	46	76.7	114	22 AAB64737	Human secreted pro
24	46	76.7	212	14 AAR32353	Cyclophilin C. Mu
25	45	75.0	108	21 AAG03830	Human secreted pro
26	45	75.0	108	22 AAM20480	Peptide #6914 enco
27	45	75.0	108	22 AAM35140	Peptide #9177 enco
28	45	75.0	114	22 AAB64736	Gene 14 human secr
29	45	75.0	145	12 AAR10763	Porcine peptidyl-p
30	45	75.0	145	16 AAR72917	Porcine peptidyl p
31	45	75.0	145	16 AAR72961	Porcine peptidyl p
32	45	75.0	163	12 AAR13726	Bovine cyclophilin
33	45	75.0	164	10 AAP90431	Calcineurin. Homo
34	45	75.0	165	19 AAW56028	Calcineurin protei
35	45	75.0	165	21 AAG03831	Human secreted pro
36	45	75.0	165	22 AAU01195	Human cyclophilin
37	45	75.0	527	22 AAB49136	D.immitis tyrosine
38	45	75.0	527	22 AAB49137	D.immitis cyclophi
39	44	73.3	60	22 AAB59530	Human secreted pro
40	44	73.3	72	22 AAB59512	Human secreted pro
41	44	73.3	141	19 AAW44367	Breast cancer-asso
42	44	73.3	141	22 AAB98719	Breast cancer-asso
43	44	73.3	163	21 AAG30405	Arabidopsis thalia
44	44	73.3	163	21 AAG50215	Arabidopsis thalia
45	44	73.3	172	21 AAG30404	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAY69924
ID AAY69924 standard; peptide; 11 AA.
XX
AC AAY69924;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #4.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP03360.
XX
PR 25-JUN-1998; 98JP-0178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumour antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumours
XX
PS Claim 4; Page 50; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours.
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 60; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKNSKPHRVI 11
 DB 1 gyknskphrvl 11

RESULT 2
 AAG00090
 ID AAG00090 standard; Protein: 166 AA.

AC AAG00090;
 DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 4171.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX Homo sapiens.

OS
 XX EP1033401-A2.
 PN 06-SEP-2000.

PD 21-FEB-2000; 2000EP-0200610.
 PF 26-FEB-1999; 99US-0122487.

PR (GEST) GENSET.
 XX Dumas Milne Edwards J, Duclert A, Giordano J;

PI WPI: 2000-500381/45.
 DR N-PSDB; AAC00096.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 13; SEQ ID 4171; 7lpp + CD-ROM; English.

PS The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.
 XX
 SQ Sequence 166 AA;

Query Match 100.0%; Score 60; DB 21; Length 166;
 Best Local Similarity 100.0%; Pred. No. 0.00078;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYKNSKPHRVI 11
 DB 87 gyknskphrvl 97

RESULT 3
 AAB73302
 ID AAB73302 standard; protein: 211 AA.

XX AAB73302;
 DT 22-MAY-2001 (first entry)

DE Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.

XX Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
 KW somatolactogenic function modulator; immunosuppression; short stature;
 KW muscle wasting; osteoporosis; HIV infection; breast cancer;
 KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia;
 KW C-terminal deletion mutant; mutein.

XX Homo sapiens.
 OS WO200113113-A1.

PN 22-FEB-2001.

PD 10-AUG-2000; 2000WO-US21789.

PF 19-AUG-1999; 99US-0149752.

PR (UTPE-) UNIV PENNSYLVANIA.

XX Clevenger CV, Ryczyn MA;

PI WPI: 2001-211249/21.

DR Novel composition for modulating somatolactogenic function, comprises
 PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
 PT B with somatolactogenic hormone -

XX Disclosure; Page -: 2lpp; English.

PS The invention relates to a composition for modulating somatolactogenic
 CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B
 CC (particularly a CypB mutant in which residues 2-12 of the mature protein
 CC are absent) or an inhibitor of the interaction of cyclophilin B with a
 CC somatolactogenic hormone (e.g., prolactin, growth hormone). The invention
 CC also relates to a method of identifying inhibitors of somatolactogenic
 CC functions using CypB and a somatolactogenic hormone, and a method for
 CC diagnosing diseases associated with abnormal somatolactogenic functions
 CC by assessing CypB levels in a sample from a patient. Cyclophilin B is
 CC useful for augmenting somatolactogenic function in the animal, and the
 CC cyclophilin B mutant or a composition comprising an inhibitor of the
 CC interaction of cyclophilin B with a somatolactogenic hormone, is useful
 CC for inhibiting somatolactogenic function in the animal. A composition
 CC comprising cyclophilin B is useful in the treatment of immunosuppression,
 CC in the treatment of short stature, muscle wasting and osteoporosis. A
 CC composition comprising cyclophilin B mutant or a composition comprising
 CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic
 CC hormone, is useful for treating HIV infection, breast and prostate
 CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
 CC sequence represents a human cyclophilin B C-terminal mutant, CypB-AIAKE.
 CC Note: The present sequence is not shown in the specification, but
 CC is derived from the wild-type CypB sequence shown on pages 17-18.

XX Sequence 211 AA;

Query Match 100.0%; Score 60; DB 22; Length 211;
 Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYKNSKFRV1 11
 |||||
 Db 87 gyknskfrv1 97
 |||||

RESULT 4
 AAB73301
 ID AAB73301 standard; protein; 216 AA.
 XX
 AC AAB73301;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Human cyclophilin B (CypB).
 XX
 KW Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
 KW somatolactogenic function modulator; immunosuppression; short stature;
 KW muscle wasting; osteoporosis; HIV infection; breast cancer;
 KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200113113-A1.
 XX
 PD 22-FEB-2001.
 XX
 PF 10-AUG-2000; 2000WO-US21789.
 XX
 PR 19-AUG-1999; 99US-0149752.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Clevenger CV, Ryczyn MA;
 XX
 DR WPI; 2001-211249/21.
 XX
 PT Novel composition for modulating somatolactogenic function, comprises
 PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
 PT B with somatolactogenic hormone
 XX
 PS Claim 1; Page 17-18; 21pp; English.
 XX
 CC The invention relates to a composition for modulating somatolactogenic
 CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B
 CC (particularly a CypB mutant in which residues 2-12 of the mature protein
 CC are absent) or an inhibitor of the interaction of cyclophilin B with a
 CC somatolactogenic hormone (e.g., prolactin, growth hormone). The invention
 CC also relates to a method of identifying inhibitors of somatolactogenic
 CC functions using CypB and a somatolactogenic hormone, and a method for
 CC diagnosing diseases associated with abnormal somatolactogenic functions
 CC by assessing CypB levels in a sample from a patient. Cyclophilin B is
 CC useful for augmenting somatolactogenic function in the animal, and
 CC cyclophilin B mutant or a composition comprising an inhibitor of the
 CC interaction of cyclophilin B with a somatolactogenic hormone, is useful
 CC for inhibiting somatolactogenic function in the animal. A composition
 CC comprising cyclophilin B is useful in the treatment of immunosuppression,
 CC in the treatment of short stature, muscle wasting and osteoporosis. A
 CC composition comprising cyclophilin B mutant or a composition comprising
 CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic
 CC hormone, is useful for treating HIV infection, breast and prostate
 CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
 CC sequence represents human cyclophilin B.
 XX
 SQ Sequence 216 AA;

Query Match 100.0%; Score 60; DB 22; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYKNSKFRV1 11

Db 87 gyknskfrv1 97
 |||||

RESULT 5

AAB43878
 ID AAB43878 standard; Protein; 291 AA.

XX
 AC AAB43878;

XX
 DT 08-FEB-2001 (first entry)

XX
 DE Human cancer associated protein sequence SEQ ID NO:1323.

XX
 KW Human; cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;
 KW antidiabetic; antisthmatic; antirheumatic; antiarthritic; antiviral;
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening.

XX
 OS Homo sapiens.

XX
 PN WO200055350-A1.

XX
 PD 21-SEP-2000.

XX
 PF 08-MAR-2000; 2000WO-US05882.

XX
 PR 12-MAR-1999; 99US-0124270.

XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX
 PI Rosen CA, Ruben SM;

XX
 DR WPI; 2000-587533/55.

XX
 DR N-PSDB; AAC78087.

XX
 PT Novel isolated nucleic acids comprising sequences encoding peptides
 PT useful for treating or diagnosing e.g. cancer -

XX
 PS Claim 11; Page 1974-1975; 2352pp; English.

XX
 CC AAC77607 to AAC78448 encode the human cancer associated proteins given
 CC in AAB43398 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnery; immunomodulator;
 CC antidiabetic; antisthmatic; antirheumatic; antiarthritic;
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
 CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
 CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention.

XX
 SQ Sequence 291 AA;

Query Match 100.0%; Score 60; DB 21; Length 291;

Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKNSKFRHVI 11
 |||||
 Db 162 gyknskfhrrvi 172

RESULT 6
 AAB49141
 ID AAB49141 standard; Protein: 171 AA.
 XX
 AC AAB49141;
 XX
 DT 08-MAR-2001 (first entry)
 XX
 DE Caenorhabditis elegans cyclophilin CeCyp-4.
 XX
 KW Cyclophilin; tyrosine; parasite.
 XX
 OS Caenorhabditis elegans.

XX US6150501-A.
 PN
 XX 21-NOV-2000.
 PD
 XX 24-FEB-1998; 98US-0028366.
 PF
 XX 24-FEB-1998; 98US-0028366.
 PR
 XX (NEW) NEW ENGLAND BIOLABS INC.
 PA
 XX Carlow CKS, Ma D, Hong X;
 PI
 XX WPI; 2001-079415/09.
 DR
 XX Novel cyclophilin, endogenous to e.g. Dirofilaria immitis, useful for
 PT identifying compounds and for treating parasitic infections which are
 PT not susceptible to cyclosporin A, comprises a tyrosine residue in
 PT drug-binding site
 XX
 PS Disclosure: Fig 2: 28pp; English.

XX The present invention relates to a cyclophilin including a tyrosine
 CC residue in the drug-binding site, and which is endogenous to the
 CC parasites Onchocerca volvulus, Brugia malayi, Dirofilaria immitis.
 CC The cyclophilin is useful for inhibiting the growth and development
 CC of parasites or for treating parasitic infections which are not
 CC susceptible to cyclosporin A. The purified tyrosine-containing,
 CC cyclophilin can be used to produce antibodies, either polyclonal or
 CC monoclonal, useful as probes to detect and/or purify related
 CC cyclophilins in other parasites.

XX Sequence 171 AA;

Query Match 80.0%; Score 48; DB 22; Length 171;
 Best Local Similarity 90.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKNSKFRHVI 11
 |||||
 Db 55 yknskfhrrvi 64

RESULT 7
 AAW80784
 ID AAW80784 standard; Protein: 180 AA.
 XX
 AC AAW80784;
 XX

DT 07-DEC-1998 (first entry)
 XX

DE D. discoideum cyclophilin (DdCyp2).
 XX
 KW Dictyostelium; Dp1; discoidin II; human Dp1; hDp1; cyclophilin; DdCyp2;
 KW bisphosphonate binding protein; calcium metabolism; cyclosporine;
 KW osteoporosis; hypercalcaemia; bone metabolism; bone metastases.
 XX
 OS Dictyostelium discoideum.
 XX
 PN WO9836064-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 13-FEB-1998; 98WO-US02709.
 XX
 PR 14-FEB-1997; 97US-0039738.
 XX
 PA (PROC) PROCTER & GAMBLE CO.
 PA (UYSH-) UNIV SHEFFIELD MED SCHOOL.
 XX
 PI Cook JS, Ebetino PH, Ibbotson KJ, JI X, Rogers MJ;
 PI Russell RGGR, Watts DJ, Xiong XJ;
 XX
 DR WPI; 1998-506311/43.
 DR N-PSDB: AAV56008.
 XX
 XX Bisphosphonate binding protein - used to treat calcium metabolism
 PT disorders, including bone metabolism, hypercalcaemia, bone
 PT metastases, and osteoporosis
 XX
 PS Claim 5; Fig 21; 98pp; English.

XX This represents the amino acid sequence of cyclophilin (DdCyp2) from the
 CC Dictyostelium discoideum Ax-2. The invention provides sequences encoding
 CC Dictyostelium Dp1, human Dp1 (hDp1) and Dictyostelium cyclophilin
 CC (DdCyp2) which are bisphosphonate binding proteins. The invention also
 CC provides methods for purifying and producing such bisphosphonate binding
 CC proteins. The bisphosphonate binding protein, or an antibody which binds
 CC to the binding protein can be used in the diagnosis of calcium metabolism
 CC disorders. They can also be used to treat calcium metabolism disorders,
 CC where the treatment is for the regulation of bone metabolism,
 CC hypercalcaemia, bone metastases, and osteoporosis, especially by
 CC regulation of bone metabolism via interaction with cyclosporine.

XX Sequence 180 AA;

Query Match 80.0%; Score 48; DB 19; Length 180;
 Best Local Similarity 80.0%; Pred. No. 0.16;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKNSKFRHVI 11
 |||||
 Db 64 yknskfhrrvi 73

RESULT 8
 AAB56701
 ID AAB56701 standard; Protein: 183 AA.
 XX
 AC AAB56701;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1279.

XX Human; prostate cancer; antigen detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW vulnery; gastrointestinal; nephrotropic; antineoplastic; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.
 XX
 OS Homo sapiens.

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XX PN WO200055174-A1.
XX PD 21-SEP-2000.
XX PF 08-MAR-2000; 2000WO-US05988.
XX PR 12-MAR-1999; 99US-0124270.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI (ROSE/) ROSEN C A.
XX PT Rosen CA, Ruben SM;
XX DR WPI; 2000-587513/55.
XX DR N-PSDB; AAF15904.
XX PS Prostate cancer associated gene sequences, referred to as prostate
XX PT cancer antigens, useful for treatment, prevention, and diagnosis of
XX PT disorders such as prostate cancer.
XX PS Claim 11; Page 1699-1700; 2338pp; English.
XX CC AAF15566 to AAF16505 encode the human prostate cancer associated
XX CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
XX CC The prostate cancer antigens can have neuroprotective, cytostatic,
XX CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
XX CC nephrotropic, antineoplastic, gynaecological and antibacterial activities,
XX CC and can be used in gene therapy. The prostate cancer antigen
XX CC polynucleotides may be used for detection of prostate cancer, chromosome
XX CC identification, as chromosome markers, and for numerous other diagnostic
XX CC or research purposes. The prostate cancer antigens may be used to treat
XX CC disorders such as neural, immune, muscular, reproductive,
XX CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
XX CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
XX CC AAB57303 represent sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 183 AA;

Query Match 80.0%; Score 48; DB 21; Length 183;
Best Local Similarity 81.8%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
   ||| | ||||
Db 65 gykgstfhrvi 75

RESULT 9
AAU01197
ID AAU01197 standard; Protein: 207 AA.
XX AC AAU01197;
XX DT 07-SEP-2001 (first entry)
XX DE Human cyclophilin D protein.
XX KW Human; adenine nucleotide translocator; ANT; MTP; cyclophilin D;
XX KW mitochondrial permeability transition pore component; cell survival;
XX KW mitochondrial core component; mitochondrial related disorder; cancer;
XX KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX OS Homo sapiens.
XX PN WO200132876-A2.
XX PD 10-MAY-2001.
XX PF 03-NOV-2000; 2000WO-US050535.
XX PR

PR 03-NOV-1999; 99US-0434354.
XX PA (MITO-) MITOKOR.
XX PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
XX PI Velicelebi G, Davis RE;
XX DR WPI; 2001-291054/30.
XX DR N-PSDB; AAS05937.
XX PT New nucleic acid expression constructs, useful for screening for agents
XX PT that alter mitochondrial permeability transition (MPT), comprises
XX PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
XX PT fused to energy transfer molecule.
XX PS Disclosure; Fig 8; 186pp; English.
XX CC The present sequence represents human cyclophilin D which is a
XX CC mitochondrial core component. Cyclophilins interact with other
XX CC mitochondrial core components e.g. adenine nucleotide translocator (ANT)
XX CC proteins to regulate MPT. ANT proteins are mitochondrial permeability
XX CC transition (MTP) pore components responsible for mediating transport
XX CC of ADP across the mitochondrial inner membrane. The present invention
XX CC relates to a novel nucleic acid expression construct comprising a
XX CC promoter operably linked to a polynucleotide encoding a mitochondrial
XX CC pore component polypeptide (e.g. ANT) fused to an energy transfer
XX CC molecule (ETW) protein (e.g. green fluorescent protein (GFP) or a FLASH
XX CC sequence). The novel expression construct can alter mitochondrial
XX CC membrane permeability transition and/or alter the interaction between
XX CC mitochondrial core components. The methods are useful for screening for
XX CC agents that alter MPT and/or cell survival. These agents are useful for
XX CC the prevention or treatment of diseases associated with altered
XX CC mitochondrial function or dysfunctional cell survival, such as
XX CC Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's
XX CC disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis,
XX CC stroke, hyperproliferative disorders e.g. cancer, and deafness.
XX SQ Sequence 207 AA;

Query Match 80.0%; Score 48; DB 22; Length 207;
Best Local Similarity 81.8%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
   ||| | ||||
Db 89 gykgstfhrvi 99

RESULT 10
AAG16463
ID AAG16463 standard; Protein: 252 AA.
XX AC AAG16463;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 17119.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.

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PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144336.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.

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PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158366.
PR 13-OCT-1999; 99US-0159299.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162143.

Query Match 80.0%; Score 48; DB 21; Length 252;
Best Local Similarity 72.7%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GYKSKFHRVI 11
   ||| | |||
Db 130 gykgsfhril 140

RESULT 11
AAG05073
ID AAG05073 standard; Protein; 254 AA.
XX AC AAG05073;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 1339.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
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PR 23-AUG-1999; 99US-0149902.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 990S-0161920.
 PR 28-OCT-1999; 990S-0161992.
 PR 28-OCT-1999; 990S-0161993.
 PR 29-OCT-1999; 990S-0162142.

Query Match 80.0%; Score 48; DB 21; Length 260;
 Best Local Similarity 72.7%; Pred. No. 0.24;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYKNSKFRHVI 11
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 Db 138 gyknsfhril 148

RESULT 15

AAW54235
 ID AAW54235 standard; peptide; 3224 AA.

XX AC AAW54235;

XX DT 10-AUG-1998 (first entry)

XX DE Human Nup358 protein.

XX KW Cervical cancer-associated protein; Cvc; tryptic peptide; human;
 detection; treatment; Nup358; nucleoporin; non-chromatin protein.

XX KW Homo sapiens.

XX PN WO9809170-A2.

XX PD 05-MAR-1998.

XX PF 19-AUG-1997; 97WO-US14526.

XX PR 30-AUG-1996; 96US-0705660.

XX PA (MATR-) MATRITECH INC.

XX PI Keesee SK, Obar R, Wu Y;

XX DR WPI; 1998-230271/20.

XX PT Detection and therapy of cervical cancer - using specific cervical
 cancer-associated proteins as targets for treatment or as indicators
 for detection

XX PS Claim 16; Page 58-65; 79pp; English.

XX CC This protein is the human nucleoporin nup358 which is used to obtain
 tryptic peptides which are used in a method for detecting cervical
 cancer. The method involves detecting the presence of a cervical
 cancer-associated protein (Cvc) in a tissue or body fluid sample. The
 Cvc is characterized as having a molecular weight of 44900-69400 Daltons
 as determined by sodium dodecyl-sulphate (SDS)-PAGE techniques and an
 isoelectric point (pI) of 5.1-6.6 as determined by standard isoelectric
 focusing techniques. The protein is further characterized as being a
 non-chromatin protein which is detectable at a higher level in a human
 cervical cancer cell than in a normal human cervical cell, as determined
 by 2D-gel electrophoresis. The methods can be used for the early and
 rapid detection of cervical cancer, for treating cervical cancers and
 for monitoring the efficacy of such treatment.

SQ Sequence 3224 AA;

Query Match 80.0%; Score 48; DB 19; Length 3224;

Best Local Similarity 81.8%; Pred. No. 3.7;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYKNSKFRHVI 11

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Db 3107 gfknsfhrvi 3117

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:03:59 ; Search time 37.64 Seconds
(without alignments)
6.576 Million cell updates/sec

Title: US-09-720-469-4
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Scoring table: BLOSUM62
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Searched: 212252 seqs, 22503292 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	126	2	US-08-482-728A-10
2	60	100.0	208	1	US-08-142-897-7
3	54	90.0	126	2	US-08-482-728A-11
4	53	88.3	161	1	US-08-145-995A-13
5	53	88.3	161	2	US-08-451-747-13
6	53	88.3	161	3	US-09-134-852-13
7	48	80.0	126	2	US-08-482-728A-12
8	48	80.0	163	1	US-08-142-897-8
9	48	80.0	164	1	US-08-145-995A-9
10	48	80.0	164	2	US-08-451-747-9
11	48	80.0	164	3	US-09-134-852-9
12	48	80.0	171	4	US-09-028-366-7
13	48	80.0	3224	2	US-08-705-660-34
14	48	80.0	3224	3	US-08-989-045-34
15	46	76.7	126	2	US-08-482-728A-15
16	46	76.7	165	1	US-08-145-995A-11
17	46	76.7	165	2	US-08-451-747-11
18	46	76.7	165	3	US-09-134-852-11
19	46	76.7	212	1	US-08-142-897-5
20	45	75.0	127	2	US-08-482-728A-9
21	45	75.0	165	1	US-08-145-995A-8
22	45	75.0	165	2	US-08-451-747-8
23	45	75.0	165	3	US-09-134-852-8
24	45	75.0	527	4	US-09-028-366-2
25	45	75.0	527	4	US-09-028-366-3
26	44	73.3	141	2	US-08-658-639-14
27	44	73.3	141	4	US-08-944-604-14

28 44 73.3 276 2 US-08-989-386-3 Sequence 3, Appli
29 44 73.3 296 4 US-08-944-604-20 Sequence 20, Appli
30 44 73.3 301 4 US-08-944-604-18 Sequence 18, Appli
31 43 71.7 123 2 US-08-482-728A-6 Sequence 6, Appli
32 43 71.7 523 2 US-08-482-728A-19 Sequence 19, Appli
33 43 71.7 523 4 US-09-028-366-4 Sequence 4, Appli
34 42 70.0 126 2 US-08-482-728A-16 Sequence 16, Appli
35 42 70.0 162 1 US-08-142-897-9 Sequence 9, Appli
36 42 70.0 162 1 US-08-145-995A-14 Sequence 14, Appli
37 42 70.0 162 2 US-08-451-747-14 Sequence 14, Appli
38 42 70.0 162 3 US-09-134-852-14 Sequence 14, Appli
39 42 70.0 171 1 US-08-145-995A-10 Sequence 10, Appli
40 42 70.0 171 2 US-08-451-747-10 Sequence 10, Appli
41 42 70.0 171 3 US-09-134-852-10 Sequence 10, Appli
42 42 70.0 176 1 US-08-145-995A-3 Sequence 3, Appli
43 42 70.0 176 2 US-08-451-747-3 Sequence 3, Appli
44 42 70.0 176 3 US-09-134-852-3 Sequence 3, Appli
45 42 70.0 269 4 US-09-028-366-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-482-728A-10
; Sequence 10, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482.728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-482-728A-10

Query Match 100.0%; Score 60; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKNSKPHRVI 11

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Db 30 GYKNSKFHRVI 40
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RESULT 2
US-08-142-897-7
; Sequence 7, Application US/08142897
; Patent No. 5447852
; GENERAL INFORMATION:
; APPLICANT: Friedman, Jeffrey S.
; APPLICANT: Weissman, Irving L.
; TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tracy J. Dunn
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 05-AUG-1991
; APPLICATION NUMBER: US 07/740,375
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION NUMBER: US 08/005,917
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-897-7

Query Match 100.0%; Score 60; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYKNSKFHRVI 11
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Db 79 GYKNSKFHRVI 89
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US-08-482-728A-11
; Sequence 11, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Pavan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tracy J. Dunn
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 05-AUG-1991
; APPLICATION NUMBER: US 07/740,375
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION NUMBER: US 08/005,917
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-482-728A-11

Query Match 90.0%; Score 54; DB 2; Length 126;
Best Local Similarity 90.9%; Pred. No. 0.0072;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 30 GYKNSKFHRVI 40
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RESULT 4
US-08-145-995A-13
; Sequence 13, Application US/08145995A
; Patent No. 5482850
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: US/08/145.995A
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
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REFERENCE/DOCKET NUMBER: 43406
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-13

Query Match 88.3%; Score 53; DB 1; Length 161;
Best Local Similarity 81.8%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNSKFHRVI 11
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Db 44 GYKSKFHRII 54

RESULT 5

US-08-451-747-13
Sequence 13, Application US/08451747
Patent No. 5821107
GENERAL INFORMATION:

APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY

TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,747

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/145,995

FILING DATE: 29-OCT-1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: WILLIAMS, GREGORY D.

REGISTRATION NUMBER: 30901

REFERENCE/DOCKET NUMBER: NEB-046-DIV

TELEPHONE: (508) 927-5054

TELEFAX: (508) 927-1705

TELEX:

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 161 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-451-747-13

Query Match 88.3%; Score 53; DB 2; Length 161;

Best Local Similarity 81.8%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNSKFHRVI 11
||| |||||:
Db 44 GYKSKFHRII 54

RESULT 6

US-09-134-852-13
Sequence 13, Application US/09134852
Patent No. 6127148
GENERAL INFORMATION:

APPLICANT: CARLOW, CLOTILDE K.S.

APPLICANT: PAGE, ANTONY

TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC

COMPOUNDS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

ADDRESSEE: CUSHMAN STREET

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/134,852

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/145,995

FILING DATE: 29-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: RESNICK, DAVID S.

REGISTRATION NUMBER: 34235

REFERENCE/DOCKET NUMBER: 43406

TELEPHONE: (617) 523-3400

TELEFAX: (617) 523-6440

TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 161 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-134-852-13

Query Match 88.3%; Score 53; DB 3; Length 161;
Best Local Similarity 81.8%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNSKFHRVI 11
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Db 44 GYKSKFHRII 54

RESULT 7

US-08-482-728A-12
Sequence 12, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:

APPLICANT: Wang, Bruce

APPLICANT: Fisher, Joseph

APPLICANT: Payan, Donald

;; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Flehr, Hohbach, Test, Albritton
;; ADDRESSEE: & Herbert
;; STREET: Four Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States
;; ZIP: 94111-4187
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/482.728A
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Silva, Robin M.
;; REGISTRATION NUMBER: 38,304
;; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989
;; TELEFAX: (415) 398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 126 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-482-728A-12

Query Match 80.0%; Score 48; DB 2; Length 126;
Best Local Similarity 81.8%; Pred No. 0.088;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
Db 30 GYKGSFHRVI 40
RESULT 8
US-08-142-897-8
; Sequence 8, Application US/08142897
; Patent No. 5447852
; GENERAL INFORMATION:
; APPLICANT: Friedman, Jeffrey S.
; APPLICANT: Weissman, Irving L.
; TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tracy J. Dunn
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,897
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/005,917
;; FILING DATE: 15-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/740,375
;; FILING DATE: 05-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dunn, Tracy D.
;; REGISTRATION NUMBER: 34,587
;; REFERENCE/DOCKET NUMBER: 5490A-92-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 163 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-142-897-8
Query Match 80.0%; Score 48; DB 1; Length 163;
Best Local Similarity 72.7%; Pred. No. 0.11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GYKNSKFHRVI 11
Db 46 GYKGSFHRVI 56
RESULT 9
US-08-145-995A-9
; Sequence 9, Application US/08145995A
; Patent No. 5482850
; GENERAL INFORMATION:
; APPLICANT: CARLOW, CLOTILDE K.S.
; APPLICANT: PAGE, ANTONY
; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,995A
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 164 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

US-08-145-995A-9

Query Match 80.0%; Score 48; DB 1; Length 164;
Best Local Similarity 72.7%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKFRVI 11
||| | |||:|
DB 47 GYKGSSFRHII 57

RESULT 10

US-08-451-747-9
; Sequence 9, Application US/08451747
; Patent No. 5821107

; GENERAL INFORMATION:

; APPLICANT: CARLOW, CLOTILDE K.S.

; APPLICANT: PAGE, ANTONY

; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC

; TITLE OF INVENTION: COMPOUNDS

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.

; STREET: 32 TOZER ROAD

; CITY: BEVERLY

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 01915

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/451.747

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/145,995

; FILING DATE: 29-OCT-1993

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: WILLIAMS, GREGORY D.

; REGISTRATION NUMBER: 30901

; REFERENCE/DOCKET NUMBER: NEB-046-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (508) 927-5054

; TELEFAX: (508) 927-1705

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 164 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-451-747-9

Query Match

80.0%; Score 48; DB 2; Length 164;

Best Local Similarity 72.7%; Pred. No. 0.12;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKFRVI 11
||| | |||:|
DB 47 GYKGSSFRHII 57

RESULT 11

US-09-134-852-9

; Sequence 9, Application US/09134852

; Patent No. 6127148

; GENERAL INFORMATION:

; APPLICANT: CARLOW, CLOTILDE K.S.

; APPLICANT: PAGE, ANTONY

; TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC

; TITLE OF INVENTION: COMPOUNDS

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

; ADDRESSEE: CUSHMAN

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/134,852

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/145,995

; FILING DATE: 29-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: RESNICK, DAVID S.

; REGISTRATION NUMBER: 34235

; REFERENCE/DOCKET NUMBER: 43406

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 523-3400

; TELEFAX: (617) 523-6440

; TELEX: 200291 STRE UR

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 164 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-09-134-852-9

Query Match

80.0%; Score 48; DB 3; Length 164;

Best Local Similarity 72.7%; Pred. No. 0.12;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKFRVI 11
||| | |||:|
DB 47 GYKGSSFRHII 57

RESULT 12

US-09-028-366-7

; Sequence 7, Application US/09028366

; Patent No. 6150501

; GENERAL INFORMATION:

; APPLICANT: CARLOW, CLOTILDE K.S.

; APPLICANT: HONG, XIOIANG

; APPLICANT: MA, DONG

; TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING

; TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: New England Biolabs, Inc.

; STREET: 32 Tozer Road

; CITY: Beverly

; STATE: MA

; COUNTRY: US

; ZIP: 01915

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028.366
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
TELEFAX: 978-927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-028-366-7

Query Match 80.0%; Score 48; DB 4; Length 171;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKNSKFRHVI 11
DB 55 YKNSKFRHVI 64

RESULT 13
US-08-705-660-34
Sequence 34, Application US/08705660
Patent No. 5858683
GENERAL INFORMATION:
APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/08/705.660
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:

LENGTH: 3224 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-705-660-34

Query Match 80.0%; Score 48; DB 2; Length 3224;
Best Local Similarity 81.8%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNSKFRHVI 11
DB 3107 GYKNSKFRHVI 3117

RESULT 14
US-08-989-045-34
Sequence 34, Application US/08989045
Patent No. 6027905
GENERAL INFORMATION:
APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
DETECTION OF CERVICAL CANCER
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/08/989.045
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3224 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-989-045-34

Query Match 80.0%; Score 48; DB 3; Length 3224;
Best Local Similarity 81.8%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNSKFRHVI 11
DB 3107 GYKNSKFRHVI 3117

RESULT 15
US-08-482-728A-15
Sequence 15, Application US/08482728A

; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-482-728A-15

Query Match 76.7%; Score 46; DB 2; Length 126;
Best Local Similarity 81.8%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GYKNSKPHRVI 11
 1111111111
Db 30 GYKGSIFHRVI 40

Search completed: January 15, 2002, 13:03:59
Job time: 215 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:06:15 ; Search time 42.04 Seconds
(without alignments)
19.931 Million cell updates/sec

Title: US-09-720-469-4
Perfect score: 60
Sequence: 1 GYKNSKFHRVI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	183	2 S71547	peptidylprolyl iso
2	60	100.0	208	1 CSHUB	peptidylprolyl iso
3	60	100.0	216	2 A56861	peptidylprolyl iso
4	54	90.0	212	2 A54204	peptidylprolyl iso
5	53	88.3	161	2 A45000	peptidylprolyl iso
6	53	88.3	173	2 T39632	peptidylprolyl iso
7	51	85.0	164	2 S63995	peptidylprolyl iso
8	50	83.3	207	2 A40516	peptidylprolyl iso
9	49	81.7	183	2 T18578	peptidylprolyl iso
10	48	80.0	137	2 S68767	peptidylprolyl iso
11	48	80.0	164	1 CSHYAC	peptidylprolyl iso
12	48	80.0	164	1 CSMSA	peptidylprolyl iso
13	48	80.0	164	1 CSRTA	peptidylprolyl iso
14	48	80.0	179	2 JT0686	peptidylprolyl iso
15	48	80.0	204	2 T21587	peptidylprolyl iso
16	48	80.0	207	2 A41581	peptidylprolyl iso
17	48	80.0	223	1 CSNCM	peptidylprolyl iso
18	48	80.0	260	2 B53422	peptidylprolyl iso
19	48	80.0	3224	1 S58884	peptidylprolyl iso
20	47	78.3	201	2 T50837	Ran-binding protei
21	47	78.3	201	2 T02489	peptidylprolyl iso
22	47	78.3	201	2 T18573	peptidylprolyl iso
23	46	76.7	162	1 CSCK	peptidylprolyl iso
24	46	76.7	165	2 B38388	peptidylprolyl iso
25	46	76.7	212	2 A40047	peptidylprolyl iso
26	45	75.0	163	1 CSBOAB	peptidylprolyl iso
27	45	75.0	163	1 CSPGA	peptidylprolyl iso
28	45	75.0	165	1 CSHUA	peptidylprolyl iso
29	45	75.0	199	2 F84808	probable peptidyl-

ALIGNMENTS

RESULT 1

S71547
peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat
N:Alternate names: cyclophilin B; PPIASE
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C:Accession: S71547
R:Ruecknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaefer, M.; Fischer, G.
submitted to the Protein Sequence Database, November 1996
A:Reference number: S71547
A:Accession: S71547
A:Molecule type: protein
A:Residues: 1-183 <RUE>

A:Experimental source: liver
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <MAT>
F:10-172/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 60; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
Db 54 GYKNSKFHRVI 64

RESULT 2

CSHUB
peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human
N:Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000
C:Accession: A39118; A39722; A40515; S65742
R:Price, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T.
Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991
A:Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl iso
A:Reference number: A39118; MUID:91156714
A:Accession: A39118
A:Molecule type: mRNA
A:Residues: 1-208 <PRI>
A:Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335
R:Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
Mol. Cell. Biol. 11, 3484-3491, 1991
A:Title: An endoplasmic reticulum-specific cyclophilin.
A:Reference number: A39722; MUID:91260697
A:Accession: A39722
A:Molecule type: mRNA
A:Residues: 1-208 <HAS>
A:Cross-references: GB:M60457; NID:g181249; PIDN:AAA35733.1; PID:g181250

30 45 75.0 225 2 S38324 peptidylprolyl iso
31 45 75.0 356 2 S62327 probable 40 kd pep
32 44 73.3 172 2 T10056 peptidylprolyl iso
33 44 73.3 172 2 T06073 peptidylprolyl iso
34 44 73.3 180 2 S51497 peptidylprolyl iso
35 44 73.3 227 2 S71849 peptidylprolyl iso
36 44 73.3 301 1 S66681 peptidylprolyl iso
37 43 71.7 165 2 S28020 peptidylprolyl iso
38 43 71.7 171 2 T27371 peptidylprolyl iso
39 43 71.7 172 2 T27882 peptidylprolyl iso
40 43 71.7 173 2 S71219 peptidylprolyl iso
41 43 71.7 173 2 T27373 peptidylprolyl iso
42 43 71.7 192 2 T27034 peptidylprolyl iso
43 43 71.7 523 2 T23003 peptidylprolyl iso
44 43 71.7 795 2 T21487 hypothetical prote
45 42 70.0 162 1 CSBY peptidylprolyl iso

R:Spik, G.; Haendler, B.; Delmas, O.; Marillier, C.; Chamoux, M.; Maes, P.; Tartar, A.; J. Biol. Chem. 266, 10735-10738, 1991
 A:Title: A novel secreted cyclophilin-like protein (SCVLP).
 A:Reference number: A40515; MUID:91250363
 A:Accession: A40515
 A:Molecule type: mRNA
 A:Residues: 'MURLSERN', 1-208 <SPI>
 A:Cross-references: GB:M63573; NID:g337998; PIDN:AAA36601.1; PID:g337999
 A:Note: the authors' translation begins at an ATG codon in poor context for initiation
 A:Note: parts of this sequence, including the amino end of the mature form, were confirmed by Marillier, C.; Allain, F.; Kouach, M.; Spik, G.
 R:Marillier, C.; Allain, F.; Kouach, M.; Spik, G.
 Biochim. Biophys. Acta 1293, 31-38, 1996
 A:Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated form
 A:Reference number: S65742; MUID:96186273
 A:Accession: S65742
 A:Molecule type: protein
 A:Residues: 26-30:203 <MAR>
 A:Experimental source: milk
 C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence of a signal sequence
 C:Comment: This protein binds to and is inhibited by the immunosuppressive drug cyclosporin A
 C:Genetics:
 A:Gene: GDB:PP1B
 A:Cross-references: GDB:127610; OMIM:123841
 A:Map position: 15q21-15q22
 C:Function:
 A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; glycoprotein; T-cell
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-203/Product: peptidylprolyl isomerase B #status experimental <MANT>
 F:35-197/Domain: cyclophilin homology <CYP>
 F:140/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 60; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.00051;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
 |||||
 Db 79 GYKNSKFHRVI 89

RESULT 3
 A56861
 peptidylprolyl isomerase (EC 5.2.1.8) Cyp-S1 precursor - mouse
 N:Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
 C:Accession: A56861; B39722; S21835
 R:Schumacher, A.; Schroter, H.; Multhaup, G.; Nordheim, A.
 Biochim. Biophys. Acta 1129, 13-22, 1991
 A:Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative signal sequence
 A:Reference number: A56861; MUID:92096454
 A:Accession: A56861
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-216 <SCH>
 A:Experimental source: teratocarcinoma F9 cells
 A:Note: sequence extracted from NCBI backbone (NCBIN:73234, NCBIP:73239)
 A:Note: parts of this sequence, including the amino end of the mature protein, were confirmed by Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
 Mol. Cell. Biol. 11, 3484-3491, 1991
 A:Title: An endoplasmic reticulum-specific cyclophilin.
 A:Reference number: A39722; MUID:91260697
 A:Accession: B39722
 A:Molecule type: mRNA
 A:Residues: 9-216 <HAS>
 A:Cross-references: GB:M60456; NID:g192864; PIDN:AAA37498.1; PID:g192865
 submitted to the EMBL Data Library, May 1991
 R:Nordheim, A.
 A:Reference number: S21835
 A:Accession: S21835

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 9-216 <NOR>
 A:Cross-references: EMBL:X58990; NID:g53034; PIDN:CAA41736.1; PID:g53035
 C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence of a signal sequence
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:34-216/Product: peptidylprolyl isomerase B #status predicted <MANT>
 F:43-205/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 60; DB 2; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.00053;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
 |||||
 Db 87 GYKNSKFHRVI 97

RESULT 4
 A54204
 peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human
 N:Alternate names: cyclophilin C
 C:Species: Homo sapiens (man)
 C:Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
 C:Accession: A54204
 R:Schneider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurlini, M.G.; Quesn
 Biochemistry 33, 8218-8224, 1994
 A:Title: Human cyclophilin C: primary structure, tissue distribution, and determination of the binding site
 A:Reference number: A54204; MUID:94304830
 A:Accession: A54204
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-212 <SCH>
 A:Cross-references: GB:S71018; NID:g547303; PIDN:AAB31350.1; PID:g547304
 A:Experimental source: kidney
 A:Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBIP:149388)
 C:Genetics:
 A:Gene: GDB:PP1C
 A:Cross-references: GDB:136196; OMIM:123842
 A:Map position: 15q21-15q22
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding
 F:37-199/Domain: cyclophilin homology <CYP>

Query Match 90.0%; Score 54; DB 2; Length 212;
 Best Local Similarity 90.9%; Pred. No. 0.0072;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
 |||||
 Db 81 GYKNSKFHRVI 91

RESULT 5
 A45000
 peptidylprolyl isomerase (EC 5.2.1.8) [similarity] - tapeworm (Echinococcus granulosus)
 N:Contains: cyclophilin
 C:Species: Echinococcus granulosus
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 08-Sep-2000
 C:Accession: A45000
 R:Lightowers, M.W.; Haralambous, A.; Rickard, M.D.
 Mol. Biochem. Parasitol. 36, 287-289, 1989
 A:Title: Amino acid sequence homology between cyclophilin and a cDNA-cloned antigen o
 A:Reference number: A45000; MUID:90014983
 A:Accession: A45000
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-161 <LIC>
 A:Cross-references: GB:J04664; NID:g158843; PIDN:AAA29058.1; PID:g158844

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:1-161/Domain: cyclophilin homology <CYP>

Query Match 88.3%; Score 53; DB 2; Length 161;
Best Local Similarity 81.8%; Pred. No. 0.0084;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYKNSKFHRVI 11
||| |||||
Db 44 GYKGSKFHRII 54

RESULT 6

peptidylprolyl isomerase (EC 5.2.1.8) u-snrnp-associated SPBC1709.04c [similarity] - f1s
T39632
N:Contains: cyclophilin
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 08-Sep-2000
C:Accession: T39632
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z21868
A:Accession: T39632
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-173 <LYN>
A:Cross-references: EMBL:AL031852; PIDN:CAA21243.1; GSPDB:GN00067; SPDB:SPBC1709.04c
A:Experimental source: strain 972h-; cosmid c1709
C:Genetics:
A:Gene: SPDB:SPBC1709.04c
A:Map position: 2
A:Introns: 10/3: 32/2: 38/2: 54/1: 76/3
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:4-173/Domain: cyclophilin homology <CYP>

Query Match 88.3%; Score 53; DB 2; Length 173;
Best Local Similarity 81.8%; Pred. No. 0.009;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYKNSKFHRVI 11
||| |||||
Db 54 GYKNSFHRII 64

RESULT 7

peptidylprolyl isomerase (EC 5.2.1.8) - German cockroach
S63995
N:Alternate names: cyclophilin
C:Species: Blattella germanica (German cockroach)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S63995
R:Martinez-Gonzalez, J.; Hegardt, F.G.
Eur. J. Biochem. 234, 284-292, 1995
A:Title: Characterization of a cDNA encoding a cytosolic peptidylprolyl cis-trans-isomerase
A:Reference number: S63995; MUID:96096751
A:Accession: S63995
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-164 <MAR>
A:Cross-references: EMBL:X87418; NID:g1235942; PIDN:CAA60869.1; PID:g1772496
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:3-164/Domain: cyclophilin homology <CYP>

Query Match 85.0%; Score 51; DB 2; Length 164;
Best Local Similarity 81.8%; Pred. No. 0.021;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYKNSKFHRVI 11
||| |||||
Db 47 GYKGSFHRVI 57

RESULT 8

A40516
peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
C:Accession: A40516
R:Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.
J. Biol. Chem. 266, 10739-10742, 1991
A:Title: S-cyclophilin. New member of the cyclophilin family associated with the secr
A:Reference number: A40516; MUID:91250364
A:Accession: A40516
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-207 <CAR>
A:Cross-references: GB:M63553; NID:g212648; PIDN:AAA49064.1; PID:g212649
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F:34-196/Domain: cyclophilin homology <CYP>

Query Match 83.3%; Score 50; DB 2; Length 207;
Best Local Similarity 81.8%; Pred. No. 0.041;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYKNSKFHRVI 11
||| |||||
Db 78 GYKGSKFHRVI 88

RESULT 9

T18578
peptidylprolyl isomerase (EC 5.2.1.8) cyp-11 [similarity] - Caenorhabditis elegans
N:Contains: cyclophilin
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C:Accession: T18578; T24269
R:Page, A.P.; MacNiven, K.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z18986
A:Accession: T18578
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-183 <PAG>
A:Cross-references: EMBL:U34955; PIDN:AAC47115.1
A:Experimental source: strain Bristol N2
R:Sims, M.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19867
A:Accession: T24269
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-183 <WIL>
A:Cross-references: EMBL:Z66499; PIDN:CAA91297.1; GSPDB:GN00020; CESP:T01B7.4
A:Experimental source: clone T01B7
C:Genetics:
A:Gene: CESP:cyp-11
A:Map position: 2
A:Introns: 34/3; 87/3; 148/1
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:16-183/Domain: cyclophilin homology <CYP>

Query Match 81.7%; Score 49; DB 2; Length 183;
Best Local Similarity 81.8%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GYKNSKFHRVI 11

DB 65 GYKNSKTHRV 75

RESULT 10

S68767
peptidylprolyl isomerase (EC 5.2.1.8) - rat (fragments)
N:Alternate names: cyclophilin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 11-Jun-1999
C:Accession: S68767
R:Tanveer, A.; Virji, S.; Andreeva, L.; Totty, N.F.; Hsuan, J.J.; Ward, J.M.; Crompton, Eur. J. Biochem. 238, 166-172, 1996
A:Title: Involvement of cyclophilin D in the activation of a mitochondrial pore by Ca(2+)
A:Reference number: S68767; MUID:96248435
A:Accession: S68767
A:Molecule type: protein
A:Residues: 1-13;14-22;23-29;30-60;61-77;78-100;101-114;115-137 <TAN>
A:Experimental source: liver
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding; mitochondrion

Query Match 80.0%; Score 48; DB 2; Length 137;
Best Local Similarity 81.8%; Pred. No. 0.064; 2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 2;

Oy 1 GYKNSKTHRV 11
||| | ||||
Db 43 GYKSTFHRV 53

RESULT 11

CSHYAC
peptidylprolyl isomerase (EC 5.2.1.8) A - Chinese hamster
N:Alternate names: cyclophilin A; cyclosporin A-binding protein A
C:Species: Cricetus griseus (Chinese hamster)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: S07597
R:Bergsma, D.J.; Sylvestre, D.
Nucleic Acids Res. 18, 200, 1990
A:Title: A Chinese hamster ovary cyclophilin cDNA sequence.
A:Reference number: S07597; MUID:90174932
A:Accession: S07597
A:Molecule type: mRNA
A:Residues: 1-164 <BER>
A:Cross-references: EMBL:X17105; NID:g49495; PIDN:CAA34961.1; PID:g49496
C:Function:
A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding; T-cell
F:3-164/Domain: cyclophilin homology <CYP>

Query Match 80.0%; Score 48; DB 1; Length 164;
Best Local Similarity 72.7%; Pred. No. 0.077;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GYKNSKTHRV 11
||| | ||||
Db 47 GYKSTFHRV 57

RESULT 12

CSMSA
peptidylprolyl isomerase (EC 5.2.1.8) A - mouse
N:Alternate names: cyclophilin A; cyclosporin A-binding protein A
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: S10327; S66416; S40742
R:Hasel, K.W.; Sutcliffe, J.G.
Nucleic Acids Res. 18, 4019, 1990
A:Title: Nucleotide sequence of a cDNA coding for mouse cyclophilin.

A:Reference number: S10327; MUID:90326555
A:Accession: S10327
A:Molecule type: mRNA
A:Residues: 1-164 <HAS>

A:Cross-references: GB:X52803; NID:g50620; PIDN:CAA36989.1; PID:g50621
R:Krummel, U.; Bang, R.; Schmidtchen, R.; Brune, K.; Bang, H.
FEBS Lett. 371, 47-51, 1995
A:Title: Cyclophilin-A is a zinc-dependent DNA binding protein in macrophages.

A:Reference number: S66416; MUID:95394146

A:Accession: S66416

A:Molecule type: protein

A:Residues: 2-21 <KRU>

A:Experimental source: nuclear cyclophilin of H4-7 cells

C:Genetics:

A:Gene: CypA

C:Function:

A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase; cyclosporin A binding; DNA binding; macrophage; T-ce

F:3-164/Domain: cyclophilin homology <CYP>

Query Match 80.0%; Score 48; DB 1; Length 164;

Best Local Similarity 72.7%; Pred. No. 0.077;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GYKNSKTHRV 11
||| | ||||
Db 47 GYKSTFHRV 57

RESULT 13

CSRTA
peptidylprolyl isomerase (EC 5.2.1.8) A - rat
N:Alternate names: 13.3K protein [misidentification]; cyclophilin A; cyclosporin A-bl
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 04-Feb-2000
C:Accession: A29819; A60036; A15632; A58859
R:Danielson, P.E.; Forss-Petter, S.; Brow, M.A.; Calavetta, L.; Douglass, J.; Milner, DNA 7, 261-267, 1988
A:Title: pIB15: A cDNA clone of the rat mRNA encoding cyclophilin.

A:Reference number: A29819; MUID:88283345

A:Accession: A29819

A:Molecule type: mRNA

A:Residues: 1-164 <DAN>

A:Cross-references: GB:M19533; NID:g203701; PIDN:AAA41009.1; PID:g203702

R:Lad, R.P.; Smith, M.A.; Hilt, D.C.

Brain Res. Mol. Brain Res. 9, 239-244, 1991

A:Title: Molecular cloning and regional distribution of rat brain cyclophilin.

A:Reference number: A60036; MUID:91232390

A:Accession: A60036

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-164 <LAD>

A:Experimental source: brain

R:Theodor, L.; Peleg, D.; Meyuhas, O.

Biochim. Biophys. Acta 826, 137-146, 1985

A:Title: P31, a mammalian housekeeping protein encoded by a multigene family containi

A:Reference number: A15632; MUID:86026347

A:Accession: A15632

A:Molecule type: mRNA

A:Residues: 100-148; MUID:M25637

A:Cross-references: EMBL:M25637

A:Note: this sequence was corrected by A58859

R:Meyuhas, O.

submitted to GenBank, December 1991

A:Reference number: A58859

A:Contents: erratum

A:Accession: A58859

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-164 <MEY>

A:Cross-references: EMBL:M25637; NID:g951424; PIDN:AAB59719.1; PID:g951425

A:Note: the submission to GenBank in entry RAPP31 is acknowledged as an unpublished error
 C:Comment: This protein belongs to a class of highly conserved proteins, abundant in the
 C:Function:
 A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; T-cell
 F:3-164/Domain: cyclophilin homology <CYP>

Query Match 80.0%; Score 48; DB 1; Length 164;
 Best Local Similarity 72.7%; Pred. No. 0.077;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYKNSKFHRVI 11
 ||| | ||| |
 DB 47 GYKGSFHRII 57

RESULT 14
 JT0686
 N:Alternate names: cyclophilin A
 C:Species: Fusarium sporotrichioides
 C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 19-Jan-2001
 C:Accession: JT0686; P0166; JT0702
 R:Chow, L.P.; Ueno, Y.; Tsugita, A.
 submitted to JIPID, June 1995
 A:Description: Amino acid sequence of peptidyl-prolyl isomerase a from Fusarium sporotrichioides
 A:Reference number: JT0686
 A:Accession: JT0686
 A:Molecule type: protein
 A:Residues: 1-179 <CHO>
 R:Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
 submitted to JIPID, May 1994
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
 A:Reference number: P0166
 A:Accession: P0166
 A:Molecule type: protein
 A:Residues: 1-41 <FKU>
 R:Chow, L.P.; Kamo, M.; Ueno, Y.; Tsugita, A.
 submitted to JIPID, August 1995
 A:Description: Amino acid sequence of peptidyl-prolyl isomerase a of Fusarium sporotrichioides
 A:Reference number: JT0702
 A:Accession: JT0702
 A:Molecule type: protein
 A:Residues: 1-179 <CH2>

C:Comment: This enzyme catalyzes interconversion of the cis and trans imino peptide bonds
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol; nucleotide binding; P-1
 F:1-179/Domain: cyclophilin homology <CYP>
 F:59-76/Domain: peptidylprolyl isomerase specific <PPI>
 F:81-88/Region: nucleotide-binding motif A (P-loop)
 F:23-172/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
 F:23/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F:28/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:131/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F:132/Binding site: substrate (Trp) #status predicted
 F:172/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predicted

Query Match 80.0%; Score 48; DB 2; Length 179;
 Best Local Similarity 72.7%; Pred. No. 0.084;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYKNSKFHRVI 11
 ||| | ||| |
 DB 58 GYKGSFHRII 68

RESULT 15
 T21587
 peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans
 N:Contains: cyclophilin

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
 C:Accession: T21587
 R:Cottage, A.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: Z19446
 A:Accession: T21587
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-204 <WIL>
 A:Cross-references: EMBL:Z92784; PIDN:CAB07192.1; GSPDB:GN00019; CESP:F31C3.1
 A:Experimental source: clone F31C3
 C:Genetics:
 A:Gene: CESP:F31C3.1
 A:Map position: 1
 A:Introns: 69/3
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase
 F:28-190/Domain: cyclophilin homology <CYP>

Query Match 80.0%; Score 48; DB 2; Length 204;
 Best Local Similarity 81.8%; Pred. No. 0.097;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYKNSKFHRVI 11
 || | |||||
 DB 72 GYPGSKFHRVI 82

Search completed: January 15, 2002, 13:06:15
 Job time: 226 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:14:59 ; Search time 24.88 Seconds
(without alignments)
16.210 Million cell updates/sec

Title: US-09-720-469-4
Perfect score: 60
Sequence: 1 GYKNSKFRHVI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

Result No.	Score	Query %	Match	Length	DB ID	Description
1	60	100.0	208	1	CYPB_HUMAN	P23284 homo sapien
2	60	100.0	208	1	CYPB_MOUSE	P4369 mus musculus
3	55	91.7	208	1	CYPB_BOVIN	P80311 bos taurus
4	54	90.0	212	1	CYPC_HUMAN	P45877 bos sapien
5	53	88.3	161	1	CYPH_ECHGR	P14088 echinococcu
6	52	86.7	208	1	CYPB_RAT	P24368 rattus norv
7	51	85.0	164	1	CYPH_BLAG	P54985 blattella g
8	50	83.3	207	1	CYPB_CHICK	P24367 gallus gall
9	49	81.7	183	1	CYPB_MOUSE	P52018 caenorhabdi
10	48	80.0	163	1	CYPH_CRITO	P14851 cricetulus
11	48	80.0	163	1	CYPH_MOUSE	P17742 mus musculus
12	48	80.0	163	1	CYPH_RAT	P10111 rattus norv
13	48	80.0	204	1	CYP5_CAEEL	P52013 caenorhabdi
14	48	80.0	206	1	CYPM_RAT	P29117 rattus norv
15	48	80.0	207	1	CYPM_HUMAN	P30405 homo sapien
16	48	80.0	223	1	CYPH_NEOCR	P10255 neurospora
17	48	80.0	260	1	CYP4_ARATH	P34791 arabidopsis
18	48	80.0	3224	1	RBP2_HUMAN	P49792 homo sapien
19	47	78.3	201	1	CYP6_CAEEL	P52014 caenorhabdi
20	46	76.7	162	1	CYPH_CANAL	P22011 candida alb
21	46	76.7	165	1	CYPH_DROME	P25007 drosophila
22	46	76.7	212	1	CYPC_MOUSE	P30412 mus musculus
23	45	75.0	163	1	CYPH_BOVIN	P04374 bos taurus
24	45	75.0	164	1	CYPH_HUMAN	P05092 homo sapien
25	45	75.0	225	1	CYPD_YEAST	P35176 saccharomyc
26	44	73.3	172	1	CYPL_ARATH	P34790 arabidopsis
27	44	73.3	172	1	CYPH_CATRO	Q39613 catharanthu
28	44	73.3	298	1	CYPE_MOUSE	Q9qz3 mus musculus
29	44	73.3	300	1	CYPE_DROME	Q9v3g3 drosophila
30	44	73.3	301	1	CYPE_HUMAN	Q9unp9 homo sapien
31	43	71.7	150	1	CYPH_ALICE	P34857 allium cepa
32	43	71.7	163	1	CYPH_UROFA	Q00660 uromyces fa
33	43	71.7	165	1	PFI_STRCH	Q06118 streptomyce

34	43	71.7	171	1	CYP2_CAEEL	P52010 caenorhabdi
35	43	71.7	171	1	CYP7_CAEEL	P52015 caenorhabdi
36	43	71.7	173	1	CYP3_CAEEL	P52011 caenorhabdi
37	43	71.7	192	1	CYP1_CAEEL	P52009 caenorhabdi
38	43	71.7	523	1	CYP4_CAEEL	P52012 caenorhabdi
39	43	71.7	1085	1	RBP2_BOVIN	P48820 bos taurus
40	42	70.0	161	1	CYPH_YEAST	P14832 saccharomyc
41	42	70.0	162	1	CYPH_SCHPO	P18253 schizosacch
42	42	70.0	171	1	CYPH_BRANA	P24525 brassica na
43	42	70.0	171	1	CYPH_LYCERS	P21568 lycopersico
44	42	70.0	172	1	CYPH_LUPLU	O49886 lupinus lut
45	42	70.0	172	1	CYPH_MAIZE	P21569 zea mays (m

ALIGNMENTS

RESULT	1
CYPB_HUMAN	
ID	CYPB_HUMAN
AC	P23284;
DT	01-NOV-1991 (Rel. 20, Created)
DT	01-NOV-1991 (Rel. 20, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE	(ROTANASE), (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-SI).
GN	PPIB OR CYPB.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 26-40.
RX	MEDLINE=91156714; PubMed=2000394;
RA	Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,
RA	Walsh C.T.;
RT	*Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-
RT	prolyl isomerase with a signal sequence.;
RL	Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91250363; PubMed=2040592;
RA	Spik G., Haendler B., Delmas O., Mariller C., Chamoux M., Maes P.,
RA	Tartar A., Montreuil J., Stedman K., Kocher H.P., Keller R.,
RA	Hiestand P.C., Movva N.R.;
RT	*A novel secreted cyclophilin-like protein (SCYLP).;
RL	J. Biol. Chem. 266:10735-10738(1991).
RN	[3]
RP	SEQUENCE OF 2-208 FROM N.A.
RX	MEDLINE=91260697; PubMed=1710767;
RA	Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
RT	*An endoplasmic reticulum-specific cyclophilin.;
RL	Mol. Cell. Biol. 11:3484-3491(1991).
RN	[4]
RP	SEQUENCE OF 64-76 AND 151-157.
RX	MEDLINE=93162043; PubMed=1286667;
RA	Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA	Vandekerckhove J.;
RT	*Microsequences of 145 proteins recorded in the two-dimensional gel
RT	protein database of normal human epidermal keratinocytes.;
RL	Electrophoresis 13:960-969(1992).
RN	[5]
RP	SUBCELLULAR LOCATION.
RX	MEDLINE=92112948; PubMed=1530944;
RA	Arber S., Krause K.-H., Caroni P.;
RT	*S-cyclophilin is retained intracellularly via a unique COOH-terminal
RT	sequence and colocalizes with the calcium storage protein
RT	calreticulin.;
RL	J. Cell Biol. 116:113-125(1992).
RN	[6]
RP	X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX	MEDLINE=94255495; PubMed=8197205;
RA	Mikol V., Kallen J., Walkinshaw M.D.;

*X-ray structure of a cyclophilin B/cyclosporin complex: comparison
with cyclophilin A and delineation of its calcineurin-binding
domain.*;
Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).
RL -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL; M60857; AAA52150.1; -;
DR EMBL; M63573; AAA36601.1; ALT_INIT.
DR EMBL; M60457; AAA35733.1; -;
DR PIR; A39118; CSHUB.
DR PIR; A40515; A40515.
DR PDB; 1CYN; 29-JAN-96.
DR Aarhus/Chent-2DPAGE; 117; NEPHGE.
DR MIM; 123841; -;
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_Isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family; 3D-structure.
FT SIGNAL 1 25
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER.
SQ SEQUENCE 208 AA; 22742 MW; A814481B7EBD4579 CRC64;

Query Match 100.0%; Score 60; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKNSKFRHVI 11
DB 79 GYKNSKFRHVI 89

RESULT 2
ID CYPB_MOUSE STANDARD; PRT; 208 AA.
AC P24369;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
GN PP1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91260697; PubMed=1710767;
RA Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
RT "An endoplasmic reticulum-specific cyclophilin.*;
RL Mol. Cell. Biol. 11:3484-3491(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RX MEDLINE=92096454; PubMed=1756174;

Schumacher A., Schroeter H., Multhaup G., Nordheim A.;
*Murine cyclophilin-SI: a variant peptidyl-prolyl isomerase with a
putative signal sequence expressed in differentiating F9 cells.*;
Biochim. Biophys. Acta 1129:13-22(1991).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL; M60456; AAA37498.1; -;
DR EMBL; X58990; CAA41736.1; -;
DR PIR; B39722; B39722.
DR PIR; S21835; S21835.
DR HSSP; P23284; 1CYN.
DR MGD; MGI:97750; Pp1b.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_Isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER
FT (BY SIMILARITY).
SQ SEQUENCE 208 AA; 22713 MW; 4B8DF5AE40BAD3A7 CRC64;

Query Match 100.0%; Score 60; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKNSKFRHVI 11
DB 79 GYKNSKFRHVI 89

RESULT 3
ID CYPB_BOVIN STANDARD; PRT; 208 AA.
AC P80311;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
GN PP1B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Carrello A., Mark P.J., House A.K., Ratajczak T.;
RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 26-71.
RC TISSUE=Brain;
RX MEDLINE=94283623; PubMed=8013656;
RA Galat A., Bouet F.;

```

RT *Cyclophilin-B is an abundant protein whose conformation is similar
RT to cyclophilin-A."
RL FEBS Lett. 347:31-36(1994).
RN [3]
RN SEQUENCE OF 26-45.
RX MEDLINE=94280416; PubMed=8010972;
RA Bose S., Muecke M., Freedman R.B.;
RT "The characterization of a cyclophilin-type peptidyl prolyl
RT cis-trans-isomerase from the endoplasmic-reticulum lumen.";
RL Biochem. J. 300:871-875(1994).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D14073; BAA03158.1; -.
DR HSSP: P23284; ICYN.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER.
FT CONFLICT 30 30 K -> G (IN REF. 3).
FT SEQUENCE 208 AA; 22701 MW; 0097C88289AF6276 CRC64;
SQ
Query Match 91.7%; Score 55; DB 1; Length 208;
Best Local Similarity 90.9%; Pred. No. 0.0026;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYKNSKFHRVI 11
DB 79 GYKDSKFHRVI 89
III:IIIIIII
RESULT 4
CYPC_HUMAN CYPC_HUMAN STANDARD; PRT; 212 AA.
AC P45877;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN C).
DE PPIC OR CYPC.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=94304830; PubMed=8031755;
RX Schneider H., Charat N., Schmitz R., Wehrli S., Mikol V.,
RA Zurini M.G., Quesnelaux V.F., Movva N.R.;
RT "Human cyclophilin C: primary structure, tissue distribution, and
RT determination of binding specificity for cyclosporins.";
RL Biochemistry 33:8218-8224(1994).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

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DR EMBL: J04664; AAA29058.1; -.
DR PIR: A45000; A45000.
DR HSP; P05092; 3C1S.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PROSITE: PS00170; CSA_PPIase_1; 1.
DR PROSITE: PS50072; CSA_PPIase_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Multigene family.
FT NON_TER 1
SQ SEQUENCE 161 AA; 17223 MW; 72661E2F4FEP466F CRC64;

Query Match      88.3%; Score 53; DB 1; Length 161;
Best Local Similarity 81.8%; Pred. No. 0.0047;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
Db 44 GYKSGKFHRII 54

RESULT 6
CYPB_RAT
ID CYPB_RAT STANDARD; PRT; 208 AA.
AC P24368;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-SI).
GN PPIB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90300692; PubMed=2194066;
RA Iwai N., Inagami T.;
RT "Molecular cloning of a complementary DNA to rat cyclophilin-like
RT protein mRNA.";
RL Kidney Int. 37:1460-1465(1990).
RN [2]
RP REVISIONS TO C-TERMINUS.
RX MEDLINE=92112948; PubMed=1530944;
RA Arber S., Krause K.-H., Caroni P.;
RT "S-cyclophilin is retained intracellularly via a unique COOH-terminal
RT sequence and colocalizes with the calcium storage protein
RT calreticulin.";
RL J. Cell Biol. 116:113-125(1992).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
DR HSP; P23284; 1CVN.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIase_1; 1.
DR PROSITE: PS50072; CSA_PPIase_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER
FT (BY SIMILARITY).
SQ SEQUENCE 208 AA; 23025 MW; 76D12AC3427FEF32 CRC64;

Query Match      86.7%; Score 52; DB 1; Length 208;
Best Local Similarity 81.8%; Pred. No. 0.0095;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
Db 44 GYKSGKFHRII 54

RESULT 7
CYPB_BLAG
ID CYPB_BLAG STANDARD; PRT; 164 AA.
AC P34985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
GN CYPB.
OS Blattella germanica (German cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberodea; Blattellidae; Blattellinae; Blattella.
OX NCBI_TaxID=6973;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96096751; PubMed=8529654;
RA Martinez-Gonzalez J., Hegardt F.G.;
RT "Characterization of a cDNA encoding a cytosolic peptidylprolyl cis-
RT trans-isomerase from Blattella germanica.";
RL Eur. J. Biochem. 234:284-292(1995).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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EMBL: X87418; CAA60869.1; -.
DR HSP; P05092; 1AWV.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIase_1; 1.
DR PROSITE: PS50072; CSA_PPIase_2; 1.
KW Cyclosporin; Isomerase; Rotamase.
SQ SEQUENCE 164 AA; 17935 MW; A5E25B574DFC99 CRC64;

Query Match      85.0%; Score 51; DB 1; Length 164;
Best Local Similarity 81.8%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
Db 47 GYKSGSRFHRVI 57

RESULT 8
CYPB_CHICK
ID CYPB_CHICK STANDARD; PRT; 207 AA.
AC P24367;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
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DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCVLP).
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91250164; PubMed=2040593;
 RA Caroni P., Rothenfluh A., McGlynn E., Schneider C.;
 RT "S-cyclophilin. New member of the cyclophilin family associated with
 the secretory pathway.";
 RL J. Biol. Chem. 266:10739-10742(1991).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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 CC -----
 DR EMBL; M63553; AAA49064.1; -;
 DR PIR; A40516; A40516.
 DR HSSP; P23284; ICYN.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIase_1; 1.
 DR PROSITE; PS50072; CSA_PPIase_2; 1.
 DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 207 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
 FT SITE 198 207 PREVENT SECRETION FROM ER
 FT (BY SIMILARITY).
 SQ SEQUENCE 207 AA; 22413 MW; D9C0C2E528E25B59 CRC64;

 Query Match 83.3%; Score 50; DB 1; Length 207;
 Best Local Similarity 81.8%; Pred. No. 0.022;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 GYKNSKFRHVI 11
 I: I I I I I I I I
 DB 78 GFKGSKFRHVI 88

 RESULT 9
 ID CYPB_CAEEL STANDARD; PRT; 183 AA.
 AC P52018;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN-11).
 DE CYP-11 OR T01B7.4.
 GN Caenorhabditis elegans.
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=96276416; PubMed=8694762;

RA Page A.P., Macniven K., Hengartner M.O.;
 RT "Cloning and biochemical characterization of the cyclophilin
 RT homologues from the free-living nematode *Caenorhabditis elegans*.";
 RL Biochem. J. 317:179-185(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Sims M.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; U34955; AAC47115.1; -;
 DR EMBL; Z66499; CAA91297.1; -;
 DR HSSP; P05092; 3CVS.
 DR WormPep; T01B7.4; CE03588.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIase_1; 1.
 DR PROSITE; PS50072; CSA_PPIase_2; 1.
 DR Isomerase; Rotamase; Multigene family.
 KW SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;
 SQ

 Query Match 81.7%; Score 49; DB 1; Length 183;
 Best Local Similarity 81.8%; Pred. No. 0.03;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GYKNSKFRHVI 11
 I: I I I I I I I I
 DB 65 GYKNCIFRHI 75

 RESULT 10
 ID CYPH_CRIL0 STANDARD; PRT; 163 AA.
 AC P14851;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
 DE (CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN).
 GN PPIA.
 OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Cricetulus.
 OX NCBI_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90174932; PubMed=2408007;
 RA Bergsma D.J., Sylvester D.;
 RT "A Chinese hamster ovary cyclophilin cDNA sequence.";
 RL Nucleic Acids Res. 18:200-200(1990).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
 CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC -----

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CC or send an email to license@isb-sib.ch).

DR EMBL: X17105; CAA34961.1; -
DR PIR: S07597; CSHAC.
DR HSSP: P05092; 3CYS.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIase_1; 1.
DR PROSITE: PS50072; CSA_PPIase_2; 1.
KW Cyclosporin; isomerase; Rotamase; Multigene family.
FT INIT_MET 0
SQ SEQUENCE 163 AA; 17768 MW; 02D44F71B8F87A1A CRC64;

Query Match 80.0%; Score 48; DB 1; Length 163;
Best Local Similarity 72.7%; Pred. No. 0.041;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKFHRVI 11
||| | |||:
DB 46 GYKGSFHRII 56

RESULT 11
CYPH_MOUSE
ID CYPH_MOUSE STANDARD; PRT: 163 AA.
AC P1742;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (SP1B).
GN PPIA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=90326555; PubMed=2197604;
RA Hazel K.W., Sutcliffe J.G.;
RT "Nucleotide sequence of a cDNA coding for mouse cyclophilin.";
RL Nucleic Acids Res. 18:4019-4019(1990).
RN [2]
RP SEQUENCE OF 1-19; 21-27 AND 76-84.
RC TISSUE=Macrophage;
RX MEDLINE=92228816; PubMed=1565646;
RA Sherry B., Varlett N., Strupp A.;
RT "Identification of cyclophilin as a proinflammatory secretory product
RT of lipopolysaccharide-activated macrophages."
RL Proc. Natl. Acad. Sci. U.S.A. 89:3511-3515(1992).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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DR EMBL: X52803; CAA36989.1; -
DR PIR: S10327; CSHSA.
DR HSSP: P05092; 3CYS.
DR SWISS-2DPAGE; P17742; MOUSE.
DR MGD: MGI:97749; Ppia.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIase_1; 1.
DR PROSITE: PS50072; CSA_PPIase_2; 1.
KW Cyclosporin; isomerase; Rotamase; Multigene family.
FT INIT_MET 0
FT CONFLICT 17 19 GRV -> TXP (IN REF. 2).
SQ SEQUENCE 163 AA; 17840 MW; AC724D44DBBF4840 CRC64;

Query Match 80.0%; Score 48; DB 1; Length 163;
Best Local Similarity 72.7%; Pred. No. 0.041;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKFHRVI 11
||| | |||:
DB 46 GYKGSFHRII 56

RESULT 12
CYPH_RAT
ID CYPH_RAT STANDARD; PRT: 163 AA.
AC P10111; P18303;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN A) (CYCLOSPORIN A-BINDING PROTEIN) (P31).
GN PPIA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=88283345; PubMed=3293952;
RA Danielson P.E., Forss-Petter S., Brow M.A., Calavetta L.,
RA Douglass J., Milner R.J., Sutcliffe J.G.;
RT "p1B15: a cDNA clone of the rat mRNA encoding cyclophilin.";
RL DNA 7:261-267(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91232390; PubMed=1851525;
RA Lad R.P., Smith M.A., Hilt D.C.;
RT "Molecular cloning and regional distribution of rat brain
RT cyclophilin.";
RL Brain Res. Mol. Brain Res. 9:239-244(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SABRA;
RX MEDLINE=86026347; PubMed=29966604;
RA Theodor L., Peleg D., Meyuhos O.;
RT "P31, a mammalian housekeeping protein encoded by a multigene family
RT containing a high proportion of pseudogenes.";
RL Biochim. Biophys. Acta 826:137-146(1985).
RN [4]
RP SEQUENCE OF 1-28.
RC TISSUE=Liver;
RX MEDLINE=92287042; PubMed=1599421;
RA Connern C.P., Halesrap A.P.;
RT "Purification and N-terminal sequencing of peptidyl-prolyl cis-trans-
RT isomerase from rat liver mitochondrial matrix reveals the existence
RT of a distinct mitochondrial cyclophilin.";

Biochem. J. 284:381-385(1992).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
CC FRAMESHIFTS.
CC
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CC -----
DR EMBL; M19533; AAA41009.1; -
DR EMBL; M25637; AAB59719.1; -
DR PIR; A15632; CSRT31.
DR PIR; A29819; CSRTA.
DR HSSP; P05092; 3CYS.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Multigene family.
FT INIT_MET 0
SQ SEQUENCE 163 AA; 17743 MW; DD16D1C980474414 CRC64;

Query Match 80.0%; Score 48; DB 1; Length 163;
Best Local Similarity 72.7%; Pred. No. 0.041;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKPHRVI 11
||| | ||| |
DB 46 GYKSSFRHII 56

RESULT 13
ID CYP5_CAEEL STANDARD; PRT; 204 AA.
AC P52013;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN-5).
GN CYP-5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=96276416; PubMed=8694762;
RA Page A.P., Macniven K., Hengartner M.O.;
RT "Cloning and biochemical characterization of the cyclophilin
RT homologues from the free-living nematode Caenorhabditis elegans.";
RL Biochem. J. 317:179-183(1996).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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CC -----
DR EMBL; U31948; AAC47126.1; -
DR HSSP; P23284; ICYN.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase; Multigene family.
SQ SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;

Query Match 80.0%; Score 48; DB 1; Length 204;
Best Local Similarity 81.8%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKPHRVI 11
||| | ||| |
DB 72 GYPGSKPHRVI 82

RESULT 14
ID CYPM_RAT STANDARD; PRT; 206 AA.
AC P29117;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR
DE (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
GN PPIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE=Skeletal muscle;
RA Price N.T., Woodfield K.Y., Halestrap A.P.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 30-58.
RC TISSUE=Liver;
RX MEDLINE=92287042; PubMed=1599421;
RA Connors C.P., Halestrap A.P.;
RT "Purification and N-terminal sequencing of peptidyl-prolyl cis-trans-
RT isomerase from rat liver mitochondrial matrix reveals the existence
RT of a distinct mitochondrial cyclophilin.";
RL Biochem. J. 284:381-385(1992).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; U68544; AAB08453.1; -
DR PIR; S23122; S23122.
DR HSSP; P05092; 3CYS.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.

DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 29 MITOCHONDRION.
FT CHAIN 30 206 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
FT VARIANT 30 39 MISSING (IN A MINOR FORM).
FT VARIANT 31 31 S -> R.
FT CONFLICT 30 30 C -> A (IN REF. 2).
SQ SEQUENCE 206 AA; 21810 MW; 69048482631B9FAD CRC64;

Query Match 80.0%; Score 48; DB 1; Length 206;
Best Local Similarity 81.8%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
 | | | | |
Db 88 GYKGSFHRVI 98

RESULT 15
CYPM_HUMAN
ID CYPM_HUMAN STANDARD; PRT; 207 AA.
AC P30405;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR
DE (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN F).
GN PPIF OR CYP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92078192; PubMed=1744118;
RA Bergsma D.J., Eder C., Gross M., Kersten H., Sylvester D.,
RA Appelbaum E., Cusimano D., Livi G.P., McLaughlin M.M., Kasyan K.,
RA Porter T.G., Silverman C., Dunnington D., Hand A., Pritchett W.P.,
RA Bossard M.J., Brandt M., Levy M.A.;
RT "The cyclophilin multigene family of peptidyl-prolyl isomerases.
Characterization of three separate human isoforms.";
RL J. Biol. Chem. 266:23204-23214(1991).
CC 1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC 1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC 1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC 1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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DR EMBL; M80254; AAA58434.1; -
DR PIR; A41581; A41581.
DR HSSP; P05092; 3CYS.
DR MIM; 604486; -
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 29 MITOCHONDRION (POTENTIAL).
FT CHAIN 30 207 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
SQ SEQUENCE 207 AA; 22040 MW; D7C76F1D4049F16A CRC64;

Query Match 80.0%; Score 48; DB 1; Length 207;
Best Local Similarity 81.8%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
 | | | | |
Db 89 GYKGSFHRVI 99

Search completed: January 15, 2002, 13:14:59
Job time: 655 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:16:25 ; Search time 78.85 Seconds
(without alignments)
20.406 Million cell updates/sec

Title: US-09-720-469-4
Perfect score: 60
Sequence: 1 GYKNSKFRHVI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_invertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	203	Q01490	Q01490 orpinomyces
2	60	100.0	208	11 O88541	O88541 rattus norv
3	60	100.0	216	4 O9BVK5	O9BVK5 homo sapien
4	60	100.0	216	11 Q9CY1	Q9CY1 mus musculus
5	54	90.0	104	13 Q98UE5	Q98UE5 xenopus lae
6	53	88.3	173	3 O74729	O74729 schizosacch
7	53	88.3	205	5 Q9W227	Q9W227 drosophila
8	51	85.0	210	5 Q9U6U5	Q9U6U5 plasmodium
9	51	85.0	210	5 Q27716	Q27716 plasmodium
10	50	83.3	164	5 Q9X225	Q9X225 lumbricus r
11	49	81.7	143	5 Q25093	Q25093 hirudo medi
12	49	81.7	173	10 Q9FW22	Q9FW22 oryza sativ
13	48	80.0	39	11 Q9R137	Q9R137 mus musculus
14	48	80.0	70	11 Q9ERB9	Q9ERB9 mesocricetu
15	48	80.0	78	5 Q9U8K2	Q9U8K2 periplaneta
16	48	80.0	147	5 Q9N717	Q9N717 leishmania
17	48	80.0	158	6 Q9N0U4	Q9N0U4 macaca mula
18	48	80.0	164	5 P91791	P91791 hemicecentrot
19	48	80.0	164	5 Q9VUD6	Q9VUD6 drosophila

20	48	80.0	164	11 Q9CWX5	Q9CWX5 mus musculu
21	48	80.0	167	11 Q9CZK9	Q9CZK9 mus musculu
22	48	80.0	171	5 Q17246	Q17246 brugia mala
23	48	80.0	171	5 Q23955	Q23955 dirofilaria
24	48	80.0	171	5 Q25633	Q25633 onchocerca
25	48	80.0	174	3 Q94184	Q94184 aspergillus
26	48	80.0	177	4 Q43447	Q43447 homo sapien
27	48	80.0	177	5 Q02614	Q02614 leishmania
28	48	80.0	177	11 Q9CQ07	Q9CQ07 mus musculu
29	48	80.0	188	11 Q9D868	Q9D868 mus musculu
30	48	80.0	197	5 Q9TW32	Q9TW32 dictyosteli
31	48	80.0	204	5 Q62190	Q62190 caenorhabdi
32	48	80.0	206	11 Q99R7	Q99R7 mus musculu
33	48	80.0	259	10 Q9FY98	Q9FY98 arabidopsis
34	48	80.0	259	10 Q9ASS6	Q9ASS6 arabidopsis
35	48	80.0	260	10 Q9FPH5	Q9FPH5 arabidopsis
36	47	78.3	162	5 Q00845	Q00845 paramesium
37	47	78.3	165	3 Q9HFU2	Q9HFU2 magnaporthe
38	47	78.3	187	5 Q9U9R3	Q9U9R3 leishmania
39	47	78.3	201	10 Q22515	Q22515 arabidopsis
40	47	78.3	201	10 Q80876	Q80876 arabidopsis
41	47	78.3	215	3 Q9HFU3	Q9HFU3 magnaporthe
42	47	78.3	3053	11 Q9ERU9	Q9ERU9 mus musculu
43	46	76.7	157	5 Q44098	Q44098 drosophila
44	46	76.7	157	5 Q44099	Q44099 drosophila
45	46	76.7	161	5 Q26565	Q26565 schistosoma

ALIGNMENTS

RESULT 1

Q01490	PRELIMINARY;	PRT;	203 AA.
ID Q01490			
AC Q01490			
DT 01-NOV-1998 (TREMREL. 08, Created)			
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)			
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)			
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)			
DE (CYCLOPHILIN B) (ROTAMASE).			
CN CYPB.			
OS Orpinomyces sp. PC-2.			
OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;			
OC Neocallimastacaceae; Orpinomyces.			
OX NCBI_FaxID=30059;			
RN [1]			
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.			
RX MEDLINE=95223986; PubMed=7708690;			
RA Chen H., Li X.-L., Ljungdahl L.G.;			
RT "A cyclophilin from the polycentric anaerobic rumen fungus Orpinomyces			
sp. strain PC-2 is highly homologous to vertebrate cyclophilin B.";			
RL Proc. Natl. Acad. Sci. U.S.A. 92:2587-2591(1995).			
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.			
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC			
PEPTIDE BONDS IN OLIGOPEPTIDES.			
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.			
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).			
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.			
DR EMBL; U17900; RAD04195.1; -.			
DR HSSP; P23284; 1CYN.			
DR Mendel; 20786; Unkp;1040;20786.			
DR InterPro; IPR002130; CSA_PPIase.			
DR Pfam; PF00160; pro-isomerase; 1.			
DR PRINTS; PR00153; CSAPPISMRASE.			
DR PROSITE; PS00170; CSA_PPIASE_1; 1.			
DR PROSITE; PS00072; CSA_PPIASE_2; 1.			
DR Isomerase; Rotamase; Signal; Cyclosporin; Endoplasmic reticulum.			
FT SIGNAL 1 22			
FT CHAIN 23 203			
FT BINDING 147 147			
FT SITE 200 203			
FT PREVENT SECRETION FROM ER (BY			
FT SIMILARITY).			
FT SEQUENCE 203 AA; 21969 MW; A5748C94305B8BE0 CRC64;			

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KW Isomerase.
SQ SEQUENCE 216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;

Query Match 100.0%; Score 60; DB 3; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
  |||
Db 73 GYKNSKFHRVI 83
  |||

RESULT 2
ID O88541 PRELIMINARY; PRT; 208 AA.
AC O88541.
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE CYCLOPHILIN B (EC 5.2.1.8).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR-KYOTO; TISSUE=KIDNEY;
RA Kainer D.B., Doris P.A.;
RT "Cyclophilin B.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; AF071225; AAC25590.1; -.
DR HSSP; P23284; ICYN.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 208 AA; 22802 MW; 02408DFA7157218C CRC64;

Query Match 100.0%; Score 60; DB 11; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
  |||
Db 79 GYKNSKFHRVI 89
  |||

RESULT 3
ID Q9BVK5 PRELIMINARY; PRT; 216 AA.
AC Q9BVK5.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE PEPTIDYL-PROLYL ISOMERASE B (CYCLOPHILIN B).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN, AND MELANOMA;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001125; AAH01125.1; -.

KW Isomerase.
SQ SEQUENCE 216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;

Query Match 100.0%; Score 60; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
  |||
Db 87 GYKNSKFHRVI 97
  |||

RESULT 4
ID Q9DCY1 PRELIMINARY; PRT; 216 AA.
AC Q9DCY1.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE PEPTIDYL-PROLYL ISOMERASE B.
GN PP1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21083660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK002357; BAB22036.1; -.
DR MGD; MGI:97750; Ppib.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
SQ SEQUENCE 216 AA; 23713 MW; CE9DAD1544AE72FE CRC64;

Query Match 100.0%; Score 60; DB 11; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
  |||
Db 87 GYKNSKFHRVI 97
  |||

RESULT 5
ID Q98UE5 PRELIMINARY; PRT; 104 AA.
AC Q98UE5.
DT 01-JUN-2001 (TREMBLrel. 17, Created)

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DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B (FRAGMENT)
 OS Xenopus laevis (African clawed frog)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Amano T., Yoshizato K.;
 RT *Isolation of genes involved in intestinal remodeling during anuran
 metamorphosis.*;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF170328; AAK11503.1; -
 KW Isomerase.
 FT NON_TER
 SQ SEQUENCE 104 AA; 11350 MW; 8F6AD1CD1C2FB3E2 CRC64;

 Query Match 90.0%; Score 54; DB 13; Length 104;
 Best Local Similarity 90.9%; Pred. No. 0 012;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 GYKNSKFRHVI 11
 DB 79 GYKNSKFRHVI 89

 RESULT 6
 ID 074729 PRELIMINARY; PRT; 173 AA.
 AC 074729;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C1709.04C (EC 5.2.1.8).
 GN SPBG1709.04C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Rajandream M.A., Barrell B.G., Rieger M.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 DR EMBL; AL031852; CAA21243.1; -
 DR HSSP; P05092; 2CPL.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 KW Hypothetical protein; Isomerase; Rotamase.
 SQ SEQUENCE 173 AA; 18905 MW; 116DA3AF3FED0655 CRC64;

Q9W227
 ID 09W227 PRELIMINARY; PRT; 205 AA.
 AC 09W227;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CG2852 PROTEIN.
 GN CG2852.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balilew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 TRANS ISOMERASE FAMILY.
 DR EMBL; AE003458; AAF46873.1; -
 DR HSSP; P23284; 1CVN.
 DR FlyBase: FBgn0034753; CG2852.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS00072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 205 AA; 22199 MW; A9CEFF88B1CC813F7 CRC64;

RESULT 7

```
Query Match      88.3%; Score 53; DB 5; Length 205;
Best Local Similarity 81.8%; Pred. No. 0.037;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNSKFHRVI 11
DB 72 GYKGSKFHRII 82
|||||

RESULT 8
Q90605 PRELIMINARY: PRT: 210 AA.
AC Q90605;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLOPHILIN.
GN CYPPL.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FCCL/HN;
RA Li X.R., Yu X.B., Luo S.H., Shan Z.X., Fang J.M., Xu J.;
RT "Sequence of cyclophilin (cyppl) gene of Plasmodium falciparum
RL (isolate FCCL/HN).";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL: AF177281; AAD55769.1; -.
DR HSP: P05092; 2CPL.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase: 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
DR PROSITE: PS00389; PTS_HPR_SER; UNKNOWN_1.
KW Isomerase; Rotamase.
SQ SEQUENCE 210 AA; 24049 MW; 778A3ICE0FD47D26 CRC64;

Query Match      85.0%; Score 51; DB 5; Length 210;
Best Local Similarity 81.8%; Pred. No. 0.089;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNSKFHRVI 11
DB 89 GYKNTTFHRVI 99
|||||

RESULT 9
Q27716 PRELIMINARY: PRT: 210 AA.
AC Q27716;
DT 01-JAN-1999 (TrEMBLrel. 09, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
GN CYP.
OS Plasmodium falciparum (isolate 3D7),
OS Plasmodium falciparum (isolate Dd2), and
OS Plasmodium falciparum (isolate hb3).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329; 57267, 137071;
RN [1]
RP SEQUENCE FROM N.A.
```

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RX MEDLINE=96123383; PubMed=8577319;
RA Reddy G.R.;
RT "Cloning and characterization of a Plasmodium falciparum cyclophilin
RT gene that is stage-specifically expressed.";
RL Mol. Biochem. Parasitol. 73:111-122(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94052193; PubMed=8234327;
RA Reddy G.R., Chakrabarti D., Schuster S.M., Perl R.J., Almira E.C.,
RA Dame J.B.;
RT "Gene sequence tags from Plasmodium falciparum genomic DNA fragments
RT prepared by the 'genese' activity of mung bean nuclease.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9867-9871(1993).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN ALL ERYTHROCYTIC STAGES, BUT
CC HIGHEST LEVEL OF EXPRESSION IN THE LATE-RING STAGE.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
DR EMBL: U10322; AAC46975.1; -.
DR HSP: P05092; 2CPL.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase: 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
DR PROSITE: PS00389; PTS_HPR_SER; UNKNOWN_1.
KW Malaria; Cyclosporin; Isomerase; Rotamase; Signal.
FT SIGNAL 1 39 POTENTIAL.
FT BINDING 40 210 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
FT BINDING 163 163 CSA (POTENTIAL).
SQ SEQUENCE 210 AA; 24049 MW; 778A359F0FD47D26 CRC64;

Query Match      85.0%; Score 51; DB 5; Length 210;
Best Local Similarity 81.8%; Pred. No. 0.089;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNSKFHRVI 11
DB 89 GYKNTTFHRVI 99
|||||

RESULT 10
Q9XZ25 PRELIMINARY: PRT: 164 AA.
AC Q9XZ25;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLOPHILIN A (EC 5.2.1.8).
GN CYP.
OS Lumbricus rubellus (Humus earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Lumbricus.
OX NCBI_TaxID=35632;
RN [1]
RP SEQUENCE FROM N.A.
RA Sturzenbaum S.R., Morgan A.J., Kille P.;
RT "Isolated from earthworms exposed to Cd-supplemented artificial
RT soil.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL: AJ238310; CAB41016.1; -.
DR HSP: P05092; 1CWL.
DR InterPro: IPR002130; CSA_PPIase.
```


DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 164 AA; 17599 MW; B30D22D66C96AE7 CRC64;

Query Match 83.3%; Score 50; DB 5; Length 164;
 Best Local Similarity 81.8%; Pred. No. 0.11;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
 I: I I I I I I I I
 Db 47 GFKGSKFHRVI 57

RESULT 11
 Q25093 PRELIMINARY; PRT; 143 AA.
 ID Q25093;
 AC Q25093;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CYCLOPHILIN-A (EC 5.2.1.8).
 HCYP.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163729; PubMed=8587897;
 RA Korneev S., Blackshaw S.E., Kaiser K., Davies J.A.;
 RT "cDNA libraries from identified neurons."
 RL Proc. R. Soc. Lond., B, Biol. Sci. 263:57-62(1996).
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 CC FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 CC TRANS ISOMERASE FAMILY.
 DR EMBL: U36797; AAB01531.1; -.
 DR HSSP; P05092; 2CPL.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 143 AA; 15398 MW; 64FFD82018480A6B CRC64;

Query Match 81.7%; Score 49; DB 5; Length 143;
 Best Local Similarity 81.8%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
 I: I I I I I I I I
 Db 26 GYKGSFHRVI 36

RESULT 12
 Q9FW22 PRELIMINARY; PRT; 173 AA.
 ID Q9FW22;
 AC Q9FW22;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE SIMILAR TO ARABIDOPSIS THALIANA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
 DE (P34791) (FRAGMENT).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartioideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-T., Liu S.-M.,
 RA Chen C.-S., Shaw J.-F.;
 RT "Oryza sativa PAC P0036D10 genomics sequence, complete sequence."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC073405; AAG03106.1; -.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 DR NON_TER 173 173
 FT NON_TER 173 173
 SQ SEQUENCE 173 AA; 19158 MW; 28EAD80F4625EB9 CRC64;

Query Match 81.7%; Score 49; DB 10; Length 173;
 Best Local Similarity 81.8%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
 I: I I I I I I I I
 Db 80 GYKGSFHRVI 90

RESULT 13
 Q9R137 PRELIMINARY; PRT; 39 AA.
 ID Q9R137;
 AC Q9R137;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CYCLOPHILIN A (FRAGMENT).
 GN PPIA OR CYPA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/OLA;
 RA Colgan J.D., Asmal M., Luban J.;
 RT "Haploinsufficient growth defects, increased Th2 cytokine production
 RT and cyclosporine resistance in mice lacking CYPA.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF171073; AAD50996.1; -.
 DR HSSP; P05092; 2CPL.
 DR MGD; MGI:97749; Ppia.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4324 MW; CB53F70E1092889C CRC64;

Query Match 80.0%; Score 48; DB 11; Length 39;
 Best Local Similarity 72.7%; Pred. No. 0.059;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
 I: I I I I I I I I
 Db 23 GYKGSFHRVI 33

RESULT 14
 Q9ERB9 PRELIMINARY; PRT; 70 AA.
 ID Q9ERB9
 AC Q9ERB9;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

01-JUN-2001 (Tremblrel. 17, Last annotation update)
CYCLOPHILIN (FRAGMENT).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
NCBI_TaxID=10036;
[1]
SEQUENCE FROM N.A.
Kirigiti P., Bai Y., Li X., Machida C.A.;
"Mesocricetus auratus cyclophilin partial cDNA coding sequence.";
Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
FOLDING OF PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
TRANS ISOMERASE FAMILY.
EMBL: AY004869; AAG00259.1; -.
InterPro: IPR002130; CSA_PPIase.
Pfam: PF00160; pro_isomerase; 1.
PRINTS: PR00153; CSAPPISMRASE.
PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE: PS50072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
FT NON_TER 1 1
NON_TER 70 70
SEQUENCE 70 AA: 7841 MW: 472374C1287ACEC9 CRC64;

Query Match 80.0%; Score 48; DB 11; Length 70;
Best Local Similarity 72.7%; Pred. No. 0.11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
||| | ||| |
Db 26 GYKGSFHRII 36

RESULT 15

Q908K2 ID Q908K2 PRELIMINARY; PRT; 78 AA.
AC Q908K2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (FRAGMENT).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ANTENNAE;
RA Renucci M., Tirard A., Matarazzo V., Belaich A., Clement J.L.;
RT "Isolation of a cDNA sequence encoding a peptidyl-prolyl cis-trans
isomerase from Periplaneta americana antennae.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
TRANS ISOMERASE FAMILY.
CC EMBL: AF041412; AAD56049.1; -.
DR HSP; P05092; 2CPL.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS50072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.

FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA: 8341 MW: DB73CC5CF97334B0 CRC64;

Query Match 80.0%; Score 48; DB 5; Length 78;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
||| | ||| |
Db 4 GYKGSFHRVI 14

Search completed: January 15, 2002, 13:16:26
Job time: 657 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:05:28 ; Search time 81.32 Seconds
(without alignments)
10.020 Million cell updates/sec

Title: US-09-720-469-5
Perfect score: 71
Sequence: 1 NFKLKHGPGW 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*

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4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	11	AAV69925	Human cyclophilin
2	71	100.0	166	AAG00090	Human secreted pro
3	71	100.0	211	AAB73302	Human cyclophilin
4	71	100.0	216	AAB73301	Human cyclophilin
5	71	100.0	291	AA193878	Human cancer assoc
6	61	85.9	212	AA1932353	Cyclophilin C, Mu
7	59	83.1	10	AAV69947	Human cyclophilin
8	52	73.2	125	AA198027	Arabidopsis thalia
9	52	73.2	152	AA1980983	Arabidopsis thalia
10	52	73.2	204	AA1980982	Arabidopsis thalia
11	52	73.2	218	AA1980981	Arabidopsis thalia

12	52	73.2	228	21	AAG18026	Arabidopsis thalia
13	52	73.2	236	21	AAG18025	Arabidopsis thalia
14	51	71.8	162	21	AAG44157	Arabidopsis thalia
15	51	71.8	176	21	AAG44156	Arabidopsis thalia
16	51	71.8	186	21	AAG44155	Arabidopsis thalia
17	51	71.8	201	21	AAG29380	Arabidopsis thalia
18	51	71.8	218	21	AAG29379	Arabidopsis thalia
19	47	66.2	254	21	AAG05073	Arabidopsis thalia
20	47	66.2	259	21	AAG05072	Arabidopsis thalia
21	46	64.8	207	22	AAU01197	Human cyclophilin
22	45	63.4	9	21	AAV69928	Human cyclophilin
23	45	63.4	191	21	AAG15070	Arabidopsis thalia
24	45	63.4	192	21	AAG48166	Arabidopsis thalia
25	45	63.4	205	21	AAG15069	Arabidopsis thalia
26	45	63.4	206	21	AAG48165	Arabidopsis thalia
27	45	63.4	252	21	AAG16463	Arabidopsis thalia
28	45	63.4	254	21	AAG16462	Arabidopsis thalia
29	45	63.4	260	21	AAG16461	Arabidopsis thalia
30	43	60.6	82	22	AAG76091	Human colon cancer
31	43	60.6	114	22	AAG64735	Gene 14 human secr
32	43	60.6	114	22	AAG64737	Human secreted pro
33	43	60.6	121	19	AAW44366	Breast cancer-asso
34	43	60.6	121	22	AAW98718	Breast cancer-asso
35	43	60.6	141	19	AAW44367	Breast cancer-asso
36	43	60.6	141	22	AAW98719	Breast cancer-asso
37	43	60.6	145	12	AA10763	Porcine peptidyl-p
38	43	60.6	145	16	AA172917	Porcine peptidyl p
39	43	60.6	145	16	AA172961	Porcine peptidyl p
40	43	60.6	163	12	AA13726	Bovine cyclophilin
41	43	60.6	164	10	AA190431	Cyclophilin, Homo
42	43	60.6	165	19	AAW56028	Calcineurin protei
43	43	60.6	165	22	AAU01195	Human cyclophilin
44	43	60.6	296	22	AAW98722	Human breast cancer
45	43	60.6	301	21	AA151902	Gene 22 human secr

ALIGNMENTS

RESULT 1

AAV69925
ID AAV69925 standard; peptide; 11 AA.
AC AAV69925;
XX
DT 11-APR-2000 (first entry)
XX Human cyclophilin B peptide fragment #5.
DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX Homo sapiens.
OS
PN WO9967288-A1.
XX
PD 29-DEC-1999.
PF
FF 24-JUN-1999; 99WO-JP03360.
XX
PR 25-JUN-1998; 96JP-0178449.
XX
PA (SUMO) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumour antigen peptides derived from cyclophilin B for treatment and
diagnosis of tumours -
XX
PS Claim 4; Page 50; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours.
 XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 71; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NFKLKHYPGW 11
 Db 1 nfkklhyppgw 11

RESULT 2
 AAG00090
 ID AAG00090 standard; Protein; 166 AA.
 XX
 AC AAG00090;
 XX
 DT 06-OCT-2000 (first entry)
 DE Human secreted protein, SEQ ID NO: 4171.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 DR N-PSDB; AAC00096.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 13; SEQ ID 4171; 7lpp + CD-ROM; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.
 XX
 SQ Sequence 166 AA;

Query Match 100.0%; Score 71; DB 21; Length 166;
 Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NFKLKHYPGW 11
 Db -127 nfkklhyppgw 137

RESULT 3
 AAB73302
 ID AAB73302 standard; protein; 211 AA.
 XX
 AC AAB73302;
 XX
 DT 22-MAY-2001 (first entry)
 DE Human cyclophilin B (CypB) C-terminal deletion mutant, CypB-AIAKE.
 XX
 KW Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
 KW somatolactogenic function modulator; immunosuppression; short stature;
 KW muscle wasting; osteoporosis; HIV infection; breast cancer;
 KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia;
 KW C-terminal deletion mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 PN WO200113113-A1.
 XX
 PD 22-FEB-2001.
 XX
 PF 10-AUG-2000; 2000WO-US21789.
 XX
 PR 19-AUG-1999; 99US-0149752.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Clevenger CV, Ryczyn MA;
 XX
 DR WPI; 2001-211249/21.
 XX
 PT Novel composition for modulating somatolactogenic function, comprises
 PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
 PT B with somatolactogenic hormone -
 XX
 PS Disclosure; Page -; 2lpp; English.
 XX
 CC The invention relates to a composition for modulating somatolactogenic
 CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B
 CC (particularly a CypB mutant in which residues 2-12 of the mature protein
 CC are absent) or an inhibitor of the interaction of cyclophilin B with a
 CC somatolactogenic hormone (e.g., prolactin, growth hormone). The invention
 CC also relates to a method of identifying inhibitors of somatolactogenic
 CC functions using CypB and a somatolactogenic hormone, and a method for
 CC diagnosing diseases associated with abnormal somatolactogenic functions
 CC by assessing CypB levels in a sample from a patient. Cyclophilin B is
 CC useful for augmenting somatolactogenic function in the animal, and
 CC cyclophilin B mutant or a composition comprising an inhibitor of the
 CC interaction of cyclophilin B with a somatolactogenic hormone, is useful
 CC for inhibiting somatolactogenic function in the animal. A composition
 CC comprising cyclophilin B is useful in the treatment of immunosuppression,
 CC in the treatment of short stature, muscle wasting and osteoporosis. A
 CC composition comprising cyclophilin B mutant or a composition comprising
 CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic
 CC hormone, is useful for treating HIV infection, breast and prostate
 CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
 CC sequence represents a human cyclophilin B C-terminal mutant, CypB-AIAKE.
 CC Note: The present sequence is not shown in the specification, but
 CC is derived from the wild-type CypB sequence shown on pages 17-18.
 XX
 SQ Sequence 211 AA;

Query Match 100.0%; Score 71; DB 22; Length 211;
 Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKHYPGW 11
|||||
Db 127 nfkikhypgw 137

RESULT 4
AAB73301
ID AAB73301 standard; protein; 216 AA.
XX AC
XX AC AAB73301;
DT 22-MAY-2001 (first entry)
XX DE
XX DE Human cyclophilin B (CypB).
XX KW Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding;
KW somatolactogenic function modulator; immunosuppression; short stature;
KW muscle wasting; osteoporosis; HIV infection; breast cancer;
KW prostate cancer; gigantism; acromegaly; hyperprolactinaemia.
XX KW
XX OS Homo sapiens.
XX WO2001131113-A1.
XX PN
XX PD 22-FEB-2001.
XX PF 10-AUG-2000; 2000WO-US21789.
XX PR 19-AUG-1999; 99US-0149752.
XX XX (UYPE-) UNIV PENNSYLVANIA.
XX PA
XX PI Clevenger CV, Rycyzyn MA;
XX WPI; 2001-211249/21.
XX DR
XX PT Novel composition for modulating somatolactogenic function, comprises
PT cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
PT B with somatolactogenic hormone -
XX PS Claim 1; Page 17-18; 21pp; English.
XX CC The invention relates to a composition for modulating somatolactogenic
CC function, comprising cyclophilin B (CypB), a mutant of cyclophilin B
CC (particularly a CypB mutant in which residues 2-12 of the mature protein
CC are absent) or an inhibitor of the interaction of cyclophilin B with a
CC somatolactogenic hormone (e.g., prolactin, growth hormone). The invention
CC also relates to a method of identifying inhibitors of somatolactogenic
CC functions using CypB and a somatolactogenic hormone, and a method for
CC diagnosing diseases associated with abnormal somatolactogenic functions
CC by assessing CypB levels in a sample from a patient. Cyclophilin B is
CC useful for augmenting somatolactogenic function in the animal, and
CC cyclophilin B mutant or a composition comprising an inhibitor of the
CC interaction of cyclophilin B with a somatolactogenic hormone, is useful
CC for inhibiting somatolactogenic function in the animal. A composition
CC comprising cyclophilin B is useful in the treatment of immunosuppression,
CC in the treatment of short stature, muscle wasting and osteoporosis. A
CC composition comprising cyclophilin B mutant or a composition comprising
CC an inhibitor of the interaction of cyclophilin B with a somatolactogenic
CC hormone, is useful for treating HIV infection, breast and prostate
CC cancer, gigantism/acromegaly, and hyperprolactinaemia. The present
CC sequence represents human cyclophilin B.
XX CC
SQ Sequence 216 AA;

Query Match 100.0%; Score 71; DB 22; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKHYPGW 11

Db 127 nfkikhypgw 137
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RESULT 5
AAB43878
ID AAB43878 standard; Protein; 291 AA.
XX AC
XX AC AAB43878;
DT 08-FEB-2001 (first entry)
XX DE
XX DE Human cancer associated protein sequence SEQ ID NO:1323.
XX KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;
KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; neurologic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.
XX KW
XX OS Homo sapiens.
XX PN WO200055350-A1.
XX XX 21-SEP-2000.
XX PF 08-MAR-2000; 2000WO-US05882.
XX PR 12-MAR-1999; 99US-0124270.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Rosen CA, Ruben SM;
XX DR WPI; 2000-587533/55.
XX DR N-PSDB; AAC78087.
XX PT Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer -
XX PS Claim 1; Page 1974-1975; 2352pp; English.
XX CC AAC77607 to AAC78448 encode the human cancer associated proteins given
CC in AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerable; immunomodulator;
CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC polynucleotides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autolimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention.
XX CC
SQ Sequence 291 AA;

Query Match 100.0%; Score 71; DB 21; Length 291;

Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NFKLKHYPGW 11
Db 202 nfkikhypgw 212
|||||

RESULT 6

AAR32353
ID AAR32353 standard; Protein; 212 AA.

XX
AC AAR32353;

XX
DT 16-JUN-1993 (first entry)

XX
DE Cyclophilin C.

XX
KW Cyclophilin C; bone marrow; stromal cell line; AC 6; interleukin-1;
IL-1; cyp A; cyp B; peptidyl-prolyl isomerase; PPIase;
KW cyclosporin A; Csa; ligand; calcineurin.

XX
OS Mus musculus.

XX
PN WO9303050-A.

XX
PD 18-FEB-1993.

XX
PF 05-AUG-1992; 92WO-US06462.

XX
PR 05-AUG-1991; 91US-0740375.

XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX
PI Friedman JS, Weissman IL;

XX
DR WPI; 1993-076431/09.

XX
DR N-PSDB; AAQ36841.

XX
PT Cyclophilin C polypeptide and nucleic acid encoding it - useful
PT for screening a tissue-specific immunosuppressive agent

XX
PS Claim 9; Page 46 + Fig 1; 63pp; English.

XX
CC A third mammalian cyclophilin, cyp C, was isolated from a cDNA
CC library prepd. from the murine bone marrow derived stromal cell line
CC AC 6. This cDNA was isolated from a substracted sub-library contg.
CC genes induced by treatment of the stromal cell line with interleukin-
CC 1 (IL-1). The message levels for cyp C show a 2-3 fold induction by
CC treatment with IL-1, and this cDNA exhibits a high level of homology
CC with known cyclophilins. Cyp C is distinct from mammalian
CC cyclophilins A and B in both sequence and tissue distribution of
CC expression. A fusion protein contg., e.g. amino acids 16-212 of cyp C
CC possesses peptidyl-prolyl isomerase (PPIase) activity which can be
CC completely inhibited by addition of cyclosporin A (Csa). These cyp C
CC fusion proteins can be used as ligands for the identification of
CC intracellular proteins which together form high affinity associations.
CC For example, the cyp C fusion protein binds to a protein of 77 kD in
CC the absence of Csa, while in the presence fo Csa it no longer binds
CC to this p77, but instead binds specifically to a protein of 55 kD,
CC identified as calcineurin (U.S.S.N.07/740175).

XX
SQ Sequence 212 AA;

Query Match 85.9%; Score 61; DB 14; Length 212;
Best Local Similarity 90.9%; Pred. No. 0.0088;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NFKLKHYPGW 11
Db 121 nfkikhypgw 131
|||||

RESULT 7

AAV69947

ID AAV69947 standard; peptide; 10 AA.

XX
AC AAV69947;

XX
DT 11-APR-2000 (first entry)

XX
DE Human cyclophilin B peptide fragment #27.

XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.

XX
OS Homo sapiens.

XX
PN WO9967288-A1.

XX
PD 29-DEC-1999.

XX
PF 24-JUN-1999; 99WO-JP03360.

XX
PR 25-JUN-1998; 98JP-0178449.

XX
PA (SUMU) SUMITOMO PHARM CO LTD.

XX
PA (ITOH/) ITOH K.

XX
PI Itoh K, Gomi S;

XX
DR WPI; 2000-116932/10.

XX
PT Tumour antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumours

XX
PS Claim 4; Page 56; 64pp; Japanese.

XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours.

XX
SQ Sequence 10 AA;

Query Match 83.1%; Score 59; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00089; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KLKHYGPGW 11

Db 1 kikhypgw 9
|||||

RESULT 8

AAAG18027

ID AAG18027 standard; Protein; 125 AA.

XX
AC AAG18027;

XX
DT 17-OCT-2000 (first entry)

XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19273.

XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX
OS Arabidopsis thaliana.

XX
PN EP1033405-A2.

XX
PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
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PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 07-JUN-1999; 99US-0137724.
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PR 18-JUN-1999; 99US-0139462.
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PR 01-JUL-1999; 99US-0142154.
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PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147192.
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PR 06-AUG-1999; 99US-0147303.
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PR 11-AUG-1999; 99US-0148319.
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PR 13-AUG-1999; 99US-0148684.
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PR 27-AUG-1999; 99US-0151066.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match      73.2%; Score 52; DB 21; Length 125;
Best Local Similarity 81.8%; Pred. No. 0.17;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHYPGW 11
Db 46 nfkltkhtgpgf 56

RESULT 9
AAG08983
ID AAG08983 standard; Protein; 152 AA.
XX AC AAG08983;
XX XX 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 6735.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.
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PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 81.8%; Pred. No. 0.21;
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XX AC AAG08982;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 6734.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PF 25-FEB-1999; 99US-0121825.
XX PF 05-MAR-1999; 99US-0123180.
XX PF 09-MAR-1999; 99US-0123548.
XX PF 23-MAR-1999; 99US-0125788.
XX PF 25-MAR-1999; 99US-0126264.
XX PF 29-MAR-1999; 99US-0126785.
XX PF 01-APR-1999; 99US-0127482.
XX PF 06-APR-1999; 99US-0128234.
XX PF 08-APR-1999; 99US-0128714.
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Query Match 73.2%; Score 52; DB 21; Length 204;

Best Local Similarity 81.8%; Pred. No. 0.29;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 125 nfkltkhtgpgf 135

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XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 6733.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX EPI033405-A2.

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Query Match 73.2%; Score 52; DB 21; Length 218;
Best Local Similarity 81.8%; Pred. No. 0.31;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 139 nfkltkgtgpf 149

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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
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PF 25-FEB-2000; 2000EP-0301439.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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ALIGNMENTS

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; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton
; ADDRESS: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482.728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
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; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-482-728A-10

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db 70 NFKLKHYPGW 80

ADDRESSEE: Flehr, Hohbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California

RESULT 2

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; Patent No. 5447852

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GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
and Uses
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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FILING DATE: 07-JUN-1995

ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000

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: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/005,917
: FILING DATE: 15-JAN-1993

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; PRIOR APPLICATION DATA:

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; PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:

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; PRIOR APPLICATION DATA:
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RESULT

US-08-142-897-5
; Sequence 5, Application US/08142897
. Patent No 5447852

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: PATENT NO.: 5497824
:
: GENERAL INFORMATION:
:
: APPLICANT: Friedman, Jeffrey S.
: APPLICANT: Weissman, Irving L.
: TITLE OF INVENTION: No. 547852el Cyclophilin, Associating Proteins
: TITLE OF INVENTION: and Uses
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
:

```

ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000

QY 1 NFKLKHYGPW 11
|||||

Qy 1 NFKLKHYPGW 11
|||||

RESULT 3

US-08-482-728A-11
; Sequence 11, Application US/08482728A
; Patent No. 5968802

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-142-897-5

Query Match 85.9%; Score 61; DB 1; Length 212;
Best Local Similarity 90.9%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPGW 11
DB 121 NFKLKHGIGW 131

RESULT 5
US-08-482-728A-12
Sequence 12, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Pavan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-12

Query Match 64.8%; Score 46; DB 2; Length 126;

Best Local Similarity 80.0%; Pred. No. 0.79;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
DB 70 NFKLKHGPG 79

RESULT 6
US-08-145-995A-15
Sequence 15, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-145-995A-15

Query Match 62.0%; Score 44; DB 1; Length 109;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
DB 39 NFKLKHGPG 48

RESULT 7
US-08-451-747-15
Sequence 15, Application US/08451747
Patent No. 5821107
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOWER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,747
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-046-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-451-747-15

Query Match 62.0%; Score 44; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NFKLKHGPG 10
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Db 39 NFKKHGTGPG 48

RESULT 8
US-09-134-852-15
Sequence 15, Application US/09134852
Patent No. 6127148
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K. S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-134-852-15

Query Match 62.0%; Score 44; DB 3; Length 109;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NFKLKHGPG 10
||| || |||
Db 39 NFKKHGTGPG 48

RESULT 9
US-08-658-639-13
Sequence 13, Application US/08658639
Patent No. 5914238
GENERAL INFORMATION:
APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,639
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-658-639-13

Query Match 60.6%; Score 43; DB 2; Length 121;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NFKLKHGPG 10
Db 26 NFILKHTGPG 35

RESULT 10
US-08-944-604-13
; Sequence 13, Application US/08944604
; Patent No. 6218131
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,604
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-944-604-13

Query Match 60.6%; Score 43; DB 4; Length 121;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NFKLKHGPG 10
Db 26 NFILKHTGPG 35

RESULT 11
US-08-482-728A-9
; Sequence 9, Application US/08482728A
; Patent No. 5968802
; GENERAL INFORMATION:
; APPLICANT: Wang, Bruce
; APPLICANT: Fisher, Joseph
; APPLICANT: Payan, Donald
; TITLE OF INVENTION: Nuclear Cyclophilin
; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,728A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-482-728A-9

Query Match 60.6%; Score 43; DB 2; Length 127;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NFKLKHGPG 10
Db 70 NFILKHTGPG 79

RESULT 12
US-08-638-639-14
; Sequence 14, Application US/08658639
; Patent No. 5914238
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,639
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C

REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-658-639-14

Query Match 60.6%; Score 43; DB 2; Length 141;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
II III III

DB 64 NFKLKHGPG 73

RESULT 13
US-08-944-604-14
Sequence 14, Application US/08944604
Patent No. 6218131
GENERAL INFORMATION:
APPLICANT: KESSEE, SUSAN
APPLICANT: OBAR, ROBERT
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-944-604-14

Query Match 60.6%; Score 43; DB 4; Length 141;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10

DB 64 NFKLKHGPG 73
II III III

RESULT 14
US-08-142-897-8
Sequence 8, Application US/08142897
Patent No. 5447852
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852el Cyclophilins, Associating Proteins
and Uses
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,897
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-142-897-8

Query Match 60.6%; Score 43; DB 1; Length 163;
Best Local Similarity 80.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
II III III

DB 86 NFKLKHGPG 95

RESULT 15
US-08-145-995A-9
Sequence 9, Application US/08145995A
Patent No. 5482850
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC
COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

us-09-720-469-5.rai

Tue Jan.15 13:46:36 2002

ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ADDRESSEE: CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/145,995A
 FILING DATE: 29-OCT-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RESNICK, DAVID S.
 REGISTRATION NUMBER: 34235
 REFERENCE/DOCKET NUMBER: 43406
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 523-3400
 TELEFAX: (617) 523-6440
 TELEX: 200291 STRE UR
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 164 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-145-995A-9

Query Match 60.6%; Score 43; DB 1; Length 164;
 Best Local Similarity 80.0%; Pred. No. 3.3;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NFKLKHYGPG 10
 || ||| |||
 Db 87 NFILKHTGPG 96

Search completed: January 15, 2002, 13:03:59
 Job time: 215 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:06:15 ; Search time 42.04 Seconds
(without alignments)
19.931 Million cell updates/sec

Title: US-09-720-469-5
Perfect score: 71
Sequence: 1 NFKLKHYPGW 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	183	2 S71547	peptidylprolyl iso
2	71	100.0	207	2 A40516	peptidylprolyl iso
3	71	100.0	208	1 CSHUB	peptidylprolyl iso
4	71	100.0	216	2 A56861	peptidylprolyl iso
5	67	94.4	201	2 T18573	peptidylprolyl iso
6	63	88.7	204	2 T21587	peptidylprolyl iso
7	61	85.9	212	2 A40047	peptidylprolyl iso
8	61	85.9	212	2 A54204	peptidylprolyl iso
9	52	73.2	204	2 T50838	peptidylprolyl iso
10	52	73.2	234	2 T49204	peptidylprolyl iso
11	51	71.8	176	2 T50767	peptidylprolyl iso
12	51	71.8	176	2 T47724	peptidylprolyl iso
13	51	71.8	201	2 T50837	peptidylprolyl iso
14	51	71.8	201	2 T02489	peptidylprolyl iso
15	49	69.0	573	1 S33212	peptidylprolyl iso
16	48	67.6	179	2 S48018	peptidylprolyl iso
17	48	67.6	183	2 T18578	peptidylprolyl iso
18	47	66.2	164	2 S33955	peptidylprolyl iso
19	46	64.8	137	2 S68767	peptidylprolyl iso
20	46	64.8	202	2 A41581	peptidylprolyl iso
21	45	63.4	192	2 T27034	peptidylprolyl iso
22	45	63.4	196	2 T52479	peptidylprolyl iso
23	45	63.4	260	2 B53422	probable gliding p
24	45	63.4	350	2 B82777	conserved hypotet
25	44	62.0	171	2 T27371	peptidylprolyl iso
26	44	62.0	172	2 T27882	peptidylprolyl iso
27	44	62.0	173	2 T27373	peptidylprolyl iso
28	43	60.6	163	1 CSBOAB	peptidylprolyl iso
29	43	60.6	163	1 CSPGA	peptidylprolyl iso

ALIGNMENTS

RESULT 1

S71547 peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat

N:Alternate names: cyclophilin B; PPIASE

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999

C:Accession: S71547

R:Ruecknagel, K.P.; Pfeifer, T.; Rahfeld, J.U.; Schaefer, M.; Fischer, G.

submitted to the Protein Sequence Database, November 1996

A:Reference number: S71547

A:Accession: S71547

A:Molecule type: protein

A:Residues: 1-183 <RUE>

A:Experimental source: liver

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase

F:1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental <MAT>
F:10-172/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 71; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NFKLKHYPGW 11

Db 94 NFKLKHYPGW 104

RESULT 2

A40516

peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999

C:Accession: A40516

J:Caroni, P.; Rothenfluh, A.; McGlynn, E.; Schneider, C.

J: Biol. Chem. 266, 10739-10742, 1991

A:Title: S-cyclophilin. New member of the cyclophilin family associated with the sec

A:Reference number: A40516; MUID:91250364

A:Accession: A40516

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-207 <CAR>

A:Cross-references: GH:M3553; NID:g212648; PID:AAA49064.1; PID:g212649

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase; cyclosporin A binding

F:34-196/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 71; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKHGPGW 11
 |||||
 Db 118 NFKLKHGPGW 128

RESULT 3
 CSHUB
 peptidylprolyl isomerase (EC 5.2.1.8) B precursor [validated] - human
 N:Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000
 C:Accession: A39118; A39722; A40515; S65742
 R:Price, E.R.; Zydowsky, L.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991
 A:Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl isomerase
 A:Reference number: A39118; A39118; MUID:911156714
 A:Accession: A39118
 A:Molecule type: mRNA
 A:Residues: 1-208 <PRI>
 A:Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335
 R:Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
 Mol. Cell. Biol. 11, 3484-3491, 1991
 A:Title: An endoplasmic reticulum-specific cyclophilin.
 A:Reference number: A39722; MUID:91260697
 A:Accession: A39722
 A:Molecule type: mRNA
 A:Residues: 1-208 <HAS>
 A:Cross-references: GB:M60457; NID:g181249; PIDN:AAA35733.1; PID:g181250
 R:Spik, G.; Haendler, B.; Delmas, O.; Marillier, C.; Chamoux, M.; Maes, P.; Tartar, A.; M
 J. Biol. Chem. 266, 10735-10738, 1991
 A:Title: A novel secreted cyclophilin-like protein (SCYLP).
 A:Reference number: A40515; MUID:91250363
 A:Accession: A40515
 A:Molecule type: mRNA
 A:Residues: 'MLRLSERN', 1-208 <SPI>
 A:Cross-references: GB:M63573; NID:g337998; PIDN:AAA36601.1; PID:g337999
 A:Note: the authors' translation begins at an ATG codon in poor context for initiation
 A:Note: parts of this sequence, including the amino end of the mature form, were confirm
 R:Marillier, C.; Allain, F.; Kovach, M.; Spik, G.
 Biochim. Biophys. Acta 1293, 31-38, 1996
 A:Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated form
 A:Reference number: S65742; MUID:96186273
 A:Accession: S65742
 A:Molecule type: protein
 A:Residues: 26-30; 203 <MAR>
 A:Experimental source: milk
 C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the presence
 C:Genetics:
 A:Gene: GDB:PP1B
 A:Cross-references: GDB:127610; OMIM:123841
 A:Map position: 15q21-15q22
 C:Function:
 A:Description: catalyzes the cis-trans isomerization of peptidylproline peptide bonds
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; glycoprotein; T-cell
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-203/Product: peptidylprolyl isomerase B #status experimental <MAR>
 F:35-197/Domain: cyclophilin homology <CYP>
 F:140/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 71; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKHGPGW 11
 |||||
 Db 119 NFKLKHGPGW 129

RESULT 4

A56861
 peptidylprolyl isomerase (EC 5.2.1.8) Cyp-S1 precursor - mouse
 N:Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
 C:Accession: A56861; B39722; S21835
 R:Schumacher, A.; Schroter, H.; Multhaup, G.; Nordheim, A.
 Biochim. Biophys. Acta 1129, 13-22, 1991
 A:Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative S
 A:Reference number: A56861; MUID:92096454
 A:Accession: A56861
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-216 <SCH>
 A:Experimental source: teratocarcinoma F9 cells
 A:Note: sequence extracted from NCBI backbone (NCBI:73234, NCBI:73239)
 R:Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G.
 Mol. Cell. Biol. 11, 3484-3491, 1991
 A:Title: An endoplasmic reticulum-specific cyclophilin.
 A:Reference number: A39722; MUID:91260697
 A:Accession: B39722
 A:Molecule type: mRNA
 A:Residues: 9-216 <HAS>
 A:Cross-references: GB:M60456; NID:g192864; PIDN:AAA37498.1; PID:g192865
 R:Nordheim, A.
 submitted to the EMBL Data Library, May 1991
 A:Reference number: S21835
 A:Accession: S21835
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 9-216 <NOR>
 A:Cross-references: EMBL:X58990; NID:g53034; PIDN:CAA41736.1; PID:g53035
 C:Comment: This protein is distinguished from peptidylprolyl isomerase A by the prese
 C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
 C:Keywords: cis-trans-isomerase; cyclosporin A binding; endoplasmic reticulum; T-cell
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:34-216/Product: peptidylprolyl isomerase B #status predicted <MAR>
 F:43-205/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 71; DB 2; Length 216;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKHGPGW 11
 |||||
 Db 127 NFKLKHGPGW 137

RESULT 5
 T18573
 peptidylprolyl isomerase (EC 5.2.1.8) precursor - Caenorhabditis elegans
 N:Alternate names: cyclophilin
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
 C:Accession: T18573; T16351
 R:Page, A.P.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: Z18981
 A:Accession: T18573
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-201 <PAG>
 A:Cross-references: EMBL:U27354; PIDN:AAC47124.1; GSPDB:GN00021; CESP:cyp-6
 A:Experimental source: strain N2
 R:Raich, A.
 submitted to the EMBL Data Library, March 1996
 A:Description: The sequence of C. elegans cosmid F42G9.
 A:Reference number: Z18498
 A:Accession: T16351
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA

A:Residues: 1-201 <TAI>
A:Cross-references: EMBL:U00051; NID:g1216305; PID:g485120; PIDN:AAA91355.1; CBSP:F4209.
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:cyp-6
A:Map position: 3
A:Introns: 66/3
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:25-187/Domain: cyclophilin homology <CYP>

Query Match 94.4%; Score 67; DB 2; Length 201;
Best Local Similarity 90.9%; Pred. No. 0.00042;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NFKLKHYPGW 11
DB 109 NFKLKHYPGW 119
||||:|||||

RESULT 6
T21587
peptidylprolyl isomerase (EC 5.2.1.8) F31C3.1 [similarity] - Caenorhabditis elegans
N:Contains: cyclophilin
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T21587
R:Cottage, A.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19446
A:Accession: T21587
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-204 <WIL>
A:Cross-references: EMBL:Z92784; PIDN:CAB07192.1; GSPDB:GN00019; CESP:F31C3.1
A:Experimental source: clone F31C3
C:Genetics:
A:Gene: CESP:F31C3.1
A:Map position: 1
A:Introns: 69/3
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:28-190/Domain: cyclophilin homology <CYP>

Query Match 88.7%; Score 63; DB 2; Length 204;
Best Local Similarity 90.9%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NFKLKHYPGW 11
DB 112 NFKLKHYPGW 122
||||:|||||

RESULT 7
A40047
peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin C) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: A40047
R:Friedman, J.; Weisman, I.
Cell 66, 799-806, 1991
A:Title: Two cytoplasmic candidates for immunophilin action are revealed by affinity for
A:Reference number: A40047; MUID:91347379
A:Accession: A40047
A:Molecule type: DNA
A:Residues: 1-212 <FRI>
A:Cross-references: NID:g192898; PIDN:AAA37511.1; PID:g192899
C:Comment: This protein binds the immunosuppressive drug cyclosporin A.
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F:37-199/Domain: cyclophilin homology <CYP>

Query Match 85.9%; Score 61; DB 2; Length 212;
Best Local Similarity 90.9%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NFKLKHYPGW 11
DB 121 NFKLKHYPGW 131
||||:|||||

RESULT 8
A54204
peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human
N:Alternate names: cyclophilin C
C:Species: Homo sapiens (man)
C:Date: 22-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A54204
R:Schneider, H.; Charara, N.; Schmitz, R.; Wehrli, S.; Mikol, V.; Zurini, M.G.; Quesn
Biochemistry 33, 8218-8224, 1994
A:Title: Human cyclophilin C: primary structure, tissue distribution, and determinati
A:Reference number: A54204; MUID:94304830
A:Accession: A54204
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-212 <SCH>
A:Cross-references: GB:S71018; NID:g547303; PIDN:AAB31350.1; PID:g547304
A:Experimental source: kidney
A:Note: sequence extracted from NCBI backbone (NCBIN:149387, NCBI:149388)
C:Genetics:
A:Gene: GDB:PPIC
A:Cross-references: GDB:136196; OMIM:123842
A:Map position: 15q21-15q22
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F:37-199/Domain: cyclophilin homology <CYP>

Query Match 85.9%; Score 61; DB 2; Length 212;
Best Local Similarity 90.9%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NFKLKHYPGW 11
DB 121 NFKLKHYPGW 131
||||:|||||

RESULT 9
T50838
peptidylprolyl isomerase (EC 5.2.1.8) ROC7 [similarity] - Arabidopsis thaliana
N:Alternate names: cyclophilin
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-Oct-2000
C:Accession: T50838
R:Jackson, K.; Soll, D.
Mol. Gen. Genet. 262, 830-8, 1999
A:Title: Mutations in a new Arabidopsis cyclophilin disrupt its interaction with prot
A:Reference number: Z25117; MUID:20092489
A:Accession: T50838
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-204 <JAC>
A:Cross-references: EMBL:AF192490; NID:g6180042; PIDN:AAF05760.1; PID:g6180043
A:Experimental source: cultivar Wassilewskija
C:Genetics:
A:Gene: ROC7
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:34-202/Domain: cyclophilin homology <CYP>

Query Match 73.2%; Score 52; DB 2; Length 204;
Best Local Similarity 81.8%; Pred. No. 0.15;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPGW 11
||||| |||
Db 125 NFKLKHGPGF 135

RESULT 10

T49204
peptidylprolyl isomerase (EC 5.2.1.8) F27K19.100 [similarity] - Arabidopsis thaliana
N:Alternate names: cyclophilin-like protein; protein F27K19.100
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 24-Oct-2000
C:Accession: T49204
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: 225014
A:Accession: T49204
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-234 <BEN>
A:Cross-references: EMBL:AL163832; GSPDB:GN00061; ATSP:F27K19.100
A:Experimental source: cultivar Columbia; BAC clone F27K19
C:Genetics:
A:Gene: ATSP:F27K19.100
A:Map position: 3
A:Introns: 27/3; 49/3; 73/1; 89/1; 164/1; 189/2
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:58-232/Domain: cyclophilin homology <CYP>

Query Match 73.2%; Score 52; DB 2; Length 234;
Best Local Similarity 81.8%; Pred. No. 0.17;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPGW 11
||||| |||
Db 155 NFKLKHGPGF 165

RESULT 11

T50767
peptidylprolyl isomerase (EC 5.2.1.8) ATCYP4 [similarity] - Arabidopsis thaliana
N:Alternate names: cyclophilin
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-Oct-2000
C:Accession: T50767
R:Saito, T.; Ashida, H.; Kawamukai, M.; Matsuda, H.; Nakagawa, T.
submitted to the EMBL Data Library, July 1995
A:Reference number: 225226
A:Accession: T50767
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-176 <SAI>
A:Cross-references: EMBL:U31370; PIDN:AAA74096.1
A:Experimental source: strain Landsberg
C:Genetics:
A:Gene: ATCYP4
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:3-171/Domain: cyclophilin homology <CYP>

Query Match 71.8%; Score 51; DB 2; Length 176;
Best Local Similarity 90.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
||||| |||
Db 94 NFKLKHGPG 103

RESULT 12

T47724
peptidylprolyl isomerase (EC 5.2.1.8) ROC2 - Arabidopsis thaliana
N:Alternate names: cytosolic cyclophilin; peptidyl-prolyl cis-trans isomerase; protei
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
C:Accession: T47724; S71220
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, April 2000
A:Reference number: 224474
A:Accession: T47724
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <BEN>
A:Cross-references: EMBL:ATF18021
A:Experimental source: cultivar Columbia; BAC clone F18021
R:Chou, I.T.; Gasser, C.S.
submitted to the EMBL Data Library, November 1995
A:Description: Characterization of cyclophilin gene family in Arabidopsis thaliana.
A:Reference number: S71219
A:Accession: S71220
A:Molecule type: DNA
A:Residues: 1-171, 'N', 173-176 <CHO>
A:Cross-references: EMBL:040400; NID:gl305456; PIDN:AAB96833.1; PID:gl305457
C:Genetics:
A:Gene: ROC2
A:Map position: 3
A:Note: F18021.30
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F:3-171/Domain: cyclophilin homology <CYP>

Query Match 71.8%; Score 51; DB 2; Length 176;
Best Local Similarity 90.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
||||| |||
Db 94 NFKLKHGPG 103

RESULT 13

T50837
peptidylprolyl isomerase (EC 5.2.1.8) CYP5 [similarity] - Arabidopsis thaliana
N:Alternate names: cyclophilin
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-Oct-2000
C:Accession: T50837
R:Saito, T.; Niwa, Y.; Ashida, H.; Tanaka, K.; Kawamukai, M.; Matsuda, H.; Nakagawa,
Plant Cell Physiol. 40, 77-87, 1999
A:Title: Expression of a gene for cyclophilin which contains an amino-terminal endopl
A:Reference number: 225256; MUID:99205703
A:Accession: T50837
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-201 <SAI>
A:Cross-references: EMBL:AF020433; PIDN:AAB71401.1
A:Experimental source: Landsberg erecta
C:Genetics:
A:Gene: CYP5
A:Introns: 22/3; 46/1; 62/1; 70/1; 131/1
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase
F:31-199/Domain: cyclophilin homology <CYP>

Query Match 71.8%; Score 51; DB 2; Length 201;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
||||| |||

us-09-720-469-5.rpr

Tue Jan 15 13:46:37 2002

QY 1 NFKLKHGPG 10
:||| |||||
Db 48 SPKXKHGPG 57

Search completed: January 15, 2002, 13:06:16
Job time: 227 sec

Db 122 NFKLKHGPG 131

RESULT 14

T02489
peptidylprolyl isomerase (EC 5.2.1.8) F23F1.12 - Arabidopsis thaliana
N:Alternate names: cyclophilin; protein At2g29960; protein F23F1.12
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C:Accession: T02489; G84702
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence.
A:Reference number: Z14675
A:Accession: T02489
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-201 <ROU>
A:Cross-references: EMBL:AC004680; NID:g3420043; PIDN:AAC31856.1; PID:g3420055
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: G84702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <STO>
A:Cross-references: GB:AE002093; NID:g3420055; PIDN:AAC31856.1; GSPDB:GNO0139
C:Genetics:
A:Gene: At2g29960
A:Map position: 2
A:Introns: 22/3; 46/1; 62/1; 70/1; 131/1
A:Note: F23F1.12
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
F:31-199/Domain: cyclophilin homology <CYP>

Query Match 71.8%; Score 51; DB 2; Length 201;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
:||||| |||
Db 122 NFKLKHGPG 131

RESULT 15

S33212
INDAL protein - fungus (Trichoderma harzianum)
C:Species: Trichoderma harzianum
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S33212
R:Vasseur, V.V.; van Montagu, M.M.; Goldman, G.G.H.
submitted to the EMBL Data Library, April 1993
A:Description: Molecular characterization of mycoparasitic-related genes of Trichoderma
A:Reference number: S33212
A:Accession: S33212
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <VAS>
A:Cross-references: EMBL:Z22594; NID:g296569; PIDN:CAA80308.1; PID:g296570
C:Superfamily: arginine permease
C:Keywords: amino acid transport; glycoprotein; transmembrane protein

Query Match 69.0%; Score 49; DB 1; Length 573;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 15, 2002, 13:14:59 ; Search time 24.88 Seconds
(without alignments)
16.210 Million cell updates/sec

Title: US-09-720-469-5
Perfect score: 71
Sequence: 1 NFKLHYGPWG 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	71	100.0	207	1 CYPB_CHICK
2	71	100.0	208	1 CYPB_BOVIN
3	71	100.0	208	1 CYPB_HUMAN
4	71	100.0	208	1 CYPB_MOUSE
5	71	100.0	208	1 CYPB_RAT
6	67	94.4	201	1 CYP6_CAEEL
7	63	88.7	204	1 CYP5_CAEEL
8	61	85.9	212	1 CYP3_CAEEL
9	61	85.9	212	1 CYP3_HUMAN
10	49	69.0	573	1 CYP3_MOUSE
11	48	67.6	183	1 INAL_TRIHA
12	47	66.2	164	1 CYPB_CAEEL
13	46	64.8	206	1 CYPB_BLAG
14	46	64.8	207	1 CYPM_RAT
15	45	63.4	192	1 CYPM_HUMAN
16	45	63.4	260	1 CYP1_CAEEL
17	44	62.0	171	1 CYP4_ARATH
18	44	62.0	171	1 CYP7_CAEEL
19	44	62.0	173	1 CYP3_CAEEL
20	43	60.6	163	1 CYP3_BOVIN
21	43	60.6	163	1 CYPH_CRILLO
22	43	60.6	163	1 CYPH_MOUSE
23	43	60.6	163	1 CYPH_RAT
24	43	60.6	164	1 CYPH_HUMAN
25	43	60.6	298	1 CYPE_MOUSE
26	43	60.6	301	1 CYPE_HUMAN
27	42	59.2	1085	1 RBP2_BOVIN
28	42	59.2	3224	1 RBP2_HUMAN
29	41	57.7	172	1 CYP1_ARATH
30	41	57.7	248	1 CYPB_VICFA
31	40	56.3	342	1 Y762_METJA
32	40	56.3	347	1 Y576_METJA
33	40	56.3	524	1 ASNS_SANAU

34	40	56.3	585	1	ASN1_LOTJA	P49092 lotus japon
35	40	56.3	585	1	ASN1_PEA	P19251 pisum sativ
36	40	56.3	585	1	ASN2_LOTJA	P49093 lotus japon
37	40	56.3	585	1	ASNS_TRIVS	O24661 triphysaria
38	40	56.3	589	1	ASNS_ASPOF	P31752 asparagus o
39	40	56.3	1184	1	XMS2_DROME	O90307 drosophila
40	39	54.9	165	1	CYPH_DROME	P25007 drosophila
41	39	54.9	582	1	ASN2_PEA	P19252 pisum sativ
42	39	54.9	860	1	SYL_PASMU	P57923 pasteurella
43	39	54.9	861	1	SYL_HAEIN	P43827 haemophilus
44	39	54.9	1451	1	SPT6_YEAST	P23615 saccharomyc
45	38	53.5	171	1	CYPH_BRANA	P24525 brassica na

ALIGNMENTS

RESULT 1
CYPB_CHICK
ID CYPB_CHICK STANDARD; PRT; 207 AA.
AC P24367;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROPAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91250364; PubMed=2040593;
RX Caroni P., Rothenfluh A., McGlynn E., Schneider C.;
RT "S-cyclophilin. New member of the cyclophilin family associated with
the secretory pathway.";
RL J. Biol. Chem. 266:10739-10742(1991).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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CC EMBL; M63553; AAA49064.1; .
CC PIR; A40516; A40516.
CC HSSP; P23284; 1CVN.
CC InterPro; IPR002130; CSA_ppiase.
CC Pfam; PF00160; pro_isomerase; 1.
CC PRINTS; PR00153; CSAPPISMRASE.
CC PROSITE; PS00170; CSA_PPIASE.1; 1.
CC PROSITE; PS50072; CSA_PPIASE.2; 1.
CC Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
CC Multigene family. 1. 24 BY SIMILARITY.
CC SIGNAL 1 24 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
CC CHAIN 25 207 PREVENT SECRETION FROM ER
CC SITE 198 207 (BY SIMILARITY).
CC SEQUENCE 207 AA; 22413 MW; D9C0C2E528E25B59 CRC64;

Query Match 100.0%; Score 71; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 3 6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NFKLKHYPGW 11
Db 118 NFKLKHYPGW 128

RESULT 2
CYPB_BOVIN STANDARD: PRT; 208 AA.
AC P80311;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP).
GN PP1B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Carrello A., Mark P.J., House A.K., Ratajczak T.;
RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 26-71.
RC TISSUE=Brain;
RX MEDLINE=94283623; PubMed=8013656;
RA Galat A., Bouet F.;
RT "Cyclophilin-B is an abundant protein whose conformation is similar
to cyclophilin-A.";
RL FEBS Lett. 347:31-36(1994).
[3]
RP SEQUENCE OF 26-45.
RX MEDLINE=94280416; PubMed=8010972;
RA Rose S., Muecke M., Freedman R.B.;
RT "The characterization of a cyclophilin-type peptidyl prolyl
cis-trans-isomerase from the endoplasmic-reticulum lumen.";
RL Biochem. J. 300:871-875(1994).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
-----
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DR EMBL: D14073; BAA03158.1; -.
DR HSP: P23284; 1CYN.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 199 208 PREVENT SECRETION FROM ER.
FT CONFLICT 30 30 K -> G (IN REF. 3).
SQ SEQUENCE 208 AA; 22701 MW; 0097C88289AF6276 CRC64;

Query Match 100.0%; Score 71; DB 1; Length 208;

Best Local Similarity 100.0%; Pred. No. 3 6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NFKLKHYPGW 11
Db 119 NFKLKHYPGW 129

RESULT 3
CYPB_HUMAN STANDARD: PRT; 208 AA.
AC P23284;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
GN PP1B OR CYPB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 26-40.
RX MEDLINE=91156714; PubMed=2000394;
RA Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D.,
Walsh C.T.;
RA "Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-
prolyl isomerase with a signal sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91250363; PubMed=2040592;
RA Spik G., Haendler B., Delmas O., Mariller C., Chamoux M., Maes P.,
Tartar A., Montreuil J., Stedman K., Kocher H.P., Keller R.,
Hiestand P.C., Movva N.R.;
RT "A novel secreted cyclophilin-like protein (SCYLP).";
RL J. Biol. Chem. 266:10735-10738(1991).
[3]
RP SEQUENCE OF 2-208 FROM N.A.
RX MEDLINE=91260697; PubMed=1710767;
RA Hasei K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
RT "An endoplasmic reticulum-specific cyclophilin.";
RL Mol. Cell. Biol. 11:3484-3491(1991).
[4]
RP SEQUENCE OF 64-76 AND 151-157.
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Geeser B., Celis J.E.,
Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
[5]
RP SUBCELLULAR LOCATION.
RX MEDLINE=92112948; PubMed=1530944;
RA Arber S., Krause K.-H., Caroni P.;
RT "S-cyclophilin is retained intracellularly via a unique COOH-terminal
sequence and colocalizes with the calcium storage protein
calreticulin.";
RL J. Cell Biol. 116:113-125(1992).
[6]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=94255495; PubMed=8197205;
RA Mikol V., Kallen J., Walkinshaw M.D.;
RT "X-ray structure of a cyclophilin B/cyclosporin complex: comparison
with cyclophilin A and delineation of its calcineurin-binding
domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.

```

CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M60587; AAA52150.1; -;
 DR EMBL: M63573; AAA36601.1; ALT_INIT.
 DR EMBL: M60457; AAA35733.1; -;
 DR PIR: A39118; CSHUB.
 DR PIR: A40515; A40515.
 DR PDB: 1CYN; 29-JAN-96.
 DR Aarhus/Ghent-2DPAGE; 117; NEPHGE.
 DR MIM: 123841; -;
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 DR Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family; 3D-structure.
 FT SIGNAL 1 25
 FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
 FT SITE 199 208 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 208 AA; 22742 MW; A814481B7EBD4579 CRC64;

Query Match 100.0%; Score 71; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKHYPGW 11
 |||||
 Db 119 NFKLKHYPGW 129

RESULT 4
 CYPB_MOUSE
 ID CYPB_MOUSE STANDARD; PRT; 208 AA.
 AC P24369;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
 GN PPIB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91260697; PubMed=1710767;
 RA Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.;
 RT "An endoplasmic reticulum-specific cyclophilin.";
 RL Mol. Cell. Biol. 11:3484-3491(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RX MEDLINE=92096454; PubMed=1756174;
 RA Schumacher A., Schroeter H., Multhaup G., Nordheim A.;
 RT "Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a
 RT putative signal sequence expressed in differentiating F9 cells.";
 RL Biochim. Biophys. Acta 1129:13-22(1991).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M60456; AAA37498.1; -;
 DR EMBL: X58990; CAA41736.1; -;
 DR PIR: B39722; B39722.
 DR PIR: S21835; S21835.
 DR HSSP: P23284; 1CYN.
 DR MGD: MGI:97750; Ppib.
 DR InterPro: IPR002130; CSA_PPIase.
 DR Pfam: PF00160; pro_isomerase; 1.
 DR PRINTS: PR00153; CSAPPISMRASE.
 DR PROSITE: PS00170; CSA_PPIASE_1; 1.
 DR PROSITE: PS50072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT CHAIN 26 208 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
 FT SITE 199 208 PREVENT SECRETION FROM ER
 (BY SIMILARITY).
 SQ SEQUENCE 208 AA; 22713 MW; 4B8DF5AE40BAD3A7 CRC64;

Query Match 100.0%; Score 71; DB 1; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKHYPGW 11
 |||||
 Db 119 NFKLKHYPGW 129

RESULT 5
 CYPB_RAT
 ID CYPB_RAT STANDARD; PRT; 208 AA.
 AC P24368;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN) (SCYLP) (CYP-S1).
 GN PPIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90300692; PubMed=2194066;
 RA Iwai N., Inagami T.;
 RT "Molecular cloning of a complementary DNA to rat cyclophilin-like
 RT protein mRNA.";
 RL Kidney Int. 37:1460-1465(1990).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RX MEDLINE=92112948; PubMed=1530944;
 RA Arber S., Krause K.-H., Caroni P.;
 RT "S-cyclophilin is retained intracellularly via a unique COOH-terminal
 RT sequence and colocalizes with the calcium storage protein
 RT calreticulin.";
 RL J. Cell Biol. 116:113-125(1992).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).

```

DR PROSITE; PS50072; CSA_PPIASE-2; 1
KW SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 201 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 6.
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 201 AA; 21864 MW; 084C5762917F958B CRC64;

Query Match 94.4%; Score 67; DB 1; Length 201;
Best Local Similarity 90.9%; Pred. No. 0.00017;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKHYPGW 11
||||:|||||
DB 109 NFKLOHYGPGW 119

RESULT 7
CYP5_CAEEL STANDARD; PRT; 204 AA.
AC PS2013;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 5 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN-5).
GN Cyp-5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
OC [1]
RN R1 SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=96276415; PubMed=8694762;
RA Page A.P., Machiven K., Hengartner M.O.;
RT Cloning and biochemical characterization of the cyclophilin
RT homologues from the free-living nematode Caenorhabditis elegans.";
RL Biochem. J. 317:179-185(1996).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----
CC EMBL; U31948; AAC47126.1; -.
CC HSSP; P23284; ICYN.
CC InterPro; IPR002130; CSA_PPIase.
CC Pfam; PF00160; pro_isomerase; 1.
CC PRINTS; PR00153; CSAPPISMRASE.
CC PROSITE; PS00170; CSA_PPIASE_1; 1.
CC PROSITE; PS50072; CSA_PPIASE-2; 1.
CC Isomerase; Rotamase; Multigene family.
SQ SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;

Query Match 88.7%; Score 63; DB 1; Length 204;
Best Local Similarity 90.9%; Pred. No. 0.00082;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHYPGW 11
|||||||||
DB 112 NFKLKHYPGW 122

RESULT 8

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CYPC_HUMAN
ID CYPC_HUMAN STANDARD; PRT; 212 AA.
AC P45877;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN C).
GN PPIC OR CYPC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed-8031755;
RX MEDLINE-94304830; PubMed-8031755;
RA Schneider H., Charara N., Schmitz R., Wehrli S., Mikol V.,
RA Zurini M.G., Quesniaux V.F., Movva N.R.;
RT "Human cyclophilin C: primary structure, tissue distribution, and
RT determination of binding specificity for cyclosporins.";
RL Biochemistry 33:8218-8224(1994).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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CC
CC EMBL; M74227; AAA37511.1; -
CC PIR; A40047; A40047.
CC HSSP; P05092; 2RMC.
CC MGI; 97751; Ppic.
CC InterPro; IPR002130; CSA_PPIase.
CC Pfam; PF00160; pro_isomerase; 1.
CC PRINTS; PR00153; CSAPPISMRASE.
CC PROSITE; PS00170; CSA_PPIASE_1; 1.
CC PROSITE; PS00072; CSA_PPIASE_2; 1.
CC Cyclosporin; Isomerase; Rotamase; Multigene family.
CC SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;
SQ
Query Match 85.9%; Score 61; DB 1; Length 212;
Best Local Similarity 90.9%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NFKLKHGPGW 11
DB 121 NFKLKHGIGW 131
RESULT 9
ID CYPC_MOUSE STANDARD; PRT; 212 AA.
AC P30412;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN C).
GN PPIC OR CYPC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94304830; PubMed-8031755;
RA Schneider H., Charara N., Schmitz R., Wehrli S., Mikol V.,
RA Zurini M.G., Quesniaux V.F., Movva N.R.;
RT "Human cyclophilin C: primary structure, tissue distribution, and
RT determination of binding specificity for cyclosporins.";
RL Biochemistry 33:8218-8224(1994).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC
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CC
CC EMBL; S71018; AAB31350.1; -
CC HSSP; P05092; 2RMC.
CC MIM; 123842; -
CC InterPro; IPR002130; CSA_PPIase.
CC Pfam; PF00160; pro_isomerase; 1.
CC PRINTS; PR00153; CSAPPISMRASE.
CC PROSITE; PS00170; CSA_PPIASE_1; 1.
CC PROSITE; PS00072; CSA_PPIASE_2; 1.
CC Cyclosporin; Isomerase; Rotamase; Multigene family.
CC SEQUENCE 212 AA; 22763 MW; 6F3DB547A2AE581B CRC64;
SQ
Query Match 85.9%; Score 61; DB 1; Length 212;
Best Local Similarity 90.9%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NFKLKHGPGW 11
DB 121 NFKLKHGIGW 131
RESULT 9
ID CYPC_MOUSE STANDARD; PRT; 212 AA.
AC P30412;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN C).
GN PPIC OR CYPC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94304830; PubMed-8031755;
RA Schneider H., Charara N., Schmitz R., Wehrli S., Mikol V.,
RA Zurini M.G., Quesniaux V.F., Movva N.R.;
RT "Human cyclophilin C: primary structure, tissue distribution, and
RT determination of binding specificity for cyclosporins.";
RL Biochemistry 33:8218-8224(1994).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC
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CC
CC EMBL; M74227; AAA37511.1; -
CC PIR; A40047; A40047.
CC HSSP; P05092; 2RMC.
CC MGI; 97751; Ppic.
CC InterPro; IPR002130; CSA_PPIase.
CC Pfam; PF00160; pro_isomerase; 1.
CC PRINTS; PR00153; CSAPPISMRASE.
CC PROSITE; PS00170; CSA_PPIASE_1; 1.
CC PROSITE; PS00072; CSA_PPIASE_2; 1.
CC Cyclosporin; Isomerase; Rotamase; Multigene family.
CC SEQUENCE 212 AA; 22794 MW; C99E7AAS5D0FA04B6 CRC64;
SQ
Query Match 85.9%; Score 61; DB 1; Length 212;
Best Local Similarity 90.9%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NFKLKHGPGW 11
DB 121 NFKLKHGIGW 131
RESULT 10
ID INAI_TRIHA STANDARD; PRT; 573 AA.
AC P34054;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE AMINO-ACID PERMEASE INDAL.
GN INDAL.
OS Trichoderma harzianum.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Trichoderma.
OX NCBI_TaxID=5544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMI 206040;
RX MEDLINE-95291429; PubMed=7773384;
RA Vasseur V.V., van Montagu M.M., Goldman G.G.H.;
RT "Trichoderma harzianum genes induced during growth on Rhizoctonia
RT solani cell walls.";
RL Microbiology 141:767-774(1995).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- INDUCTION: DURING MYCOPARASITISM.
CC -!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
CC
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CC -----
DR EMBL; Z22594; CAA80308.1; -.
DR PIR; S33212; S33212.
DR InterPro; IPR002293; AA_rel_permease_1.
DR Pfam; PF00324; aa_permeases; 1.
DR PROSITE; PS00218; AMINO-ACID_PERMEASE_1; 1.
KW Transport; Amino-acid transport; Transmembrane.
FT TRANSMEM 72 92 POTENTIAL.
FT TRANSMEM 99 117 POTENTIAL.
FT TRANSMEM 176 200 POTENTIAL.
FT TRANSMEM 212 229 POTENTIAL.
FT TRANSMEM 257 280 POTENTIAL.
FT TRANSMEM 296 315 POTENTIAL.
FT TRANSMEM 351 371 POTENTIAL.
FT TRANSMEM 398 415 POTENTIAL.
FT TRANSMEM 425 444 POTENTIAL.
FT TRANSMEM 470 494 POTENTIAL.
FT TRANSMEM 511 527 POTENTIAL.
SQ SEQUENCE 573 AA; 62850 MW; 5FB0A806934DB55D CRC64;

Query Match 69.0%; Score 49; DB 1; Length 573;
Best Local Similarity 80.0%; Pred. No. 0.55;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NPKLKHYPGP 10
DB 48 SPKKHYPGP 57

RESULT 11
CYPB_CAEEL STANDARD; PRT; 183 AA.
AC P52018;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 11 (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN-11).
GN CYP-11 OR T01B7.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=96276416; PubMed=8694762;
RA Page A.P., Macniven K., Hengartner M.O.;
RT Cloning and biochemical characterization of the cyclophilin
RL homologues from the free-living nematode Caenorhabditis elegans.;
RL Biochem. J. 317:179-185(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Sims M.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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CC -----
DR EMBL; U34955; AAC47115.1; -.
DR
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DR EMBL; Z66499; CAA91297.1; -.
DR HSSP; P05092; 3CYS.
DR WormPep; T01B7.4; CF03588.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase; Multigene family.
SQ SEQUENCE 183 AA; 20193 MW; 23549C922828C533 CRC64;

Query Match 67.6%; Score 48; DB 1; Length 183;
Best Local Similarity 80.0%; Pred. No. 0.27;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NPKLKHYPGP 10
DB 105 NPELKHYPGP 114

RESULT 12
CYPH_BLAQE STANDARD; PRT; 164 AA.
AC P54985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN).
GN CYPB.
OS Blattella germanica (German cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blattellidae; Blattellinae; Blattella.
OX NCBI_TaxID=6973;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96096751; PubMed=8529654;
RA Martinez-Gonzalez J., Hegardt F.G.;
RT Trans-isomerase from Blattella germanica.;
RL Eur. J. Biochem. 234:284-292(1995).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES SOME
CC OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
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CC -----
DR EMBL; X87418; CAA60869.1; -.
DR HSSP; P05092; IAWV.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase.
SQ SEQUENCE 164 AA; 17935 MW; A5E25B574DFDC99 CRC64;

Query Match 66.2%; Score 47; DB 1; Length 164;
Best Local Similarity 80.0%; Pred. No. 0.36;
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Matches 8: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
11:11111111

Db 87 NFQLKHTGPG 96

RESULT 13

CYPM_RAT

ID CYPM_RAT STANDARD; PRT; 206 AA.

AC P29117;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR

DE (EC 5.2.1.8) (PIPIASE) (ROTAMASE) (CYCLOPHILIN F).

GN PP1F.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WISTAR; TISSUE=Skeletal muscle;

RA Price N.T., Woodfield K.Y., Halestrap A.P.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 30-58.

RC TISSUE=Liver;

RX MEDLINE=92287042; PubMed=1599421;

RA Connern C.P., Halestrap A.P.;

RT "Purification and N-terminal sequencing of peptidyl-prolyl cis-trans-

isomerase from rat liver mitochondrial matrix reveals the existence

of a distinct mitochondrial cyclophilin.";

RL Biochem. J. 284:381-385(1992).

CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.

CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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DR EMBL; U68544; AAB08453.1; -

DR PIR; S23122; S23122.

DR HSSP; P05092; 3CYS.

DR InterPro; IPR002130; CSA_PPIase.

DR Pfam; PF00160; pro_isomerase; 1.

DR PRINTS; PR00153; CSAPPISMRASE.

DR PROSITE; PS00170; CSA_PPIASE_1; 1.

DR PROSITE; PS50072; CSA_PPIASE_2; 1.

KW Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;

KW Transit peptide.

FT TRANSIT 1 29 MITOCHONDRION.

FT CHAIN 30 206 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.

FT VARIANT 30 39 MISSING (IN A MINOR FORM).

FT VARIANT 31 31 S -> R.

FT CONFLICT 30 30 C -> A (IN REF. 2).

FT SEQUENCE 206 AA; 21810 MW; 69048482631B9FAD CRC64;

Query Match

Best Local Similarity 64.8%; Score 46; DB 1; Length 206;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
11:11111111

Db 128 NFKLKHGPG 137

RESULT 14

CYPM_HUMAN

ID CYPM_HUMAN STANDARD; PRT; 207 AA.

AC P30405;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR

DE (EC 5.2.1.8) (PIPIASE) (ROTAMASE) (CYCLOPHILIN F).

GN PP1F OR CYP3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92078192; PubMed=1744118;

RA Bergsma D.J., Eder C., Gross M., Kersten H., Sylvestre D.,

RA Appelbaum E., Cusimano D., Livi G.P., McLaughlin M.M., Kasyan K.,

RA Porter T.G., Silverman C., Dunnington D., Hand A., Pritchett W.P.,

RA Bossard M.J., Brandt M., Levy M.A.;

RT "The cyclophilin multigene family of peptidyl-prolyl isomerases.

RT Characterization of three separate human isoforms.";

RL J. Biol. Chem. 266:23204-23214(1991).

CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.

CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

PEPTIDE BONDS IN OLIGOPEPTIDES.

CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.

CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.

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DR EMBL; M80254; AAA58434.1; -

DR PIR; A41581; A41581.

DR HSSP; P05092; 3CYS.

DR MIM; 604486; -

DR InterPro; IPR002130; CSA_PPIase.

DR Pfam; PF00160; pro_isomerase; 1.

DR PRINTS; PR00153; CSAPPISMRASE.

DR PROSITE; PS00170; CSA_PPIASE_1; 1.

DR PROSITE; PS50072; CSA_PPIASE_2; 1.

KW Cyclosporin; Isomerase; Rotamase; Multigene family; Mitochondrion;

KW Transit peptide.

FT TRANSIT 1 29 MITOCHONDRION (POTENTIAL).

FT CHAIN 30 207 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.

FT SEQUENCE 207 AA; 22040 MW; D7C76FD4049F16A CRC64;

Query Match

Best Local Similarity 64.8%; Score 46; DB 1; Length 207;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
11:11111111

Db 129 NFKLKHGPG 138

RESULT 15

CYPL_CAEEL

ID CYPL_CAEEL STANDARD; PRT; 192 AA.

AC P52009;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
DE (CYCLOPHILIN-1).
GN CYP-1 OR Y49A3A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RC STRAIN-BRISTOL N2;
RX MEDLINE=96276416; PubMed=8694762;
RA Page A.P., Macniven K., Hengartner M.O.;
RT "Cloning and biochemical characterization of the cyclophilin
RT homologues from the free-living nematode Caenorhabditis elegans.";
RL Biochem. J. 317:179-185(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA McMurray A.A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U30943; AAC47116.1; -
DR EMBL: AL033512; CAA22075.1; -
DR HSP: P05092; 1AWV.
DR WormPep: Y49A3A.5; CE22213.
DR InterPro: IPR002130; CSA_PPIase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PPIASE_1; 1.
DR PROSITE: PS50072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase; Multigene family.
SQ SEQUENCE 192 AA; 20710 MW; C2094D91809ECE85 CRC64;

Query Match 63.4%; Score 45; DB 1; Length 192;
Best Local Similarity 80.0%; Pred. NO. 0.92;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 NFKLKHYPG 10
DB 112 NFDLKHYPG 121

Search completed: January 15, 2002, 13:14:59
Job time: 655 sec

Result No.	Query No.	Score	Query %		Length	DB	ID	Description
			Match					
1	1	71	100.0	208	11	O88541	O88541 rattus norv	
2	2	71	100.0	216	4	Q9BVK5	Q9BVK5 homo sapien	
3	3	71	100.0	216	11	Q9DCY1	Q9DCY1 mus musculu	
4	4	63	88.7	120	5	Q917V3	Q917V3 drosophila	
5	5	63	88.7	204	5	O62190	O62190 caenorhabdi	
6	6	63	88.7	205	5	Q9W227	Q9W227 drosophila	
7	7	63	88.7	220	5	O44073	O44073 tachypneus	
8	8	55	77.5	213	5	Q27774	Q27774 schistosoma	
9	9	54	76.1	87	6	Q29278	Q29278 sus scrofa	
10	10	52	73.2	204	10	Q9SP02	Q9SP02 arabidopsis	
11	11	52	73.2	213	5	Q26551	Q26551 schistosoma	
12	12	52	73.2	234	10	O9LY53	O9LY53 arabidopsis	
13	13	51	71.8	143	5	Q25093	Q25093 hirudo medi	
14	14	51	71.8	176	10	Q38867	Q38867 arabidopsis	
15	15	51	71.8	176	10	Q38901	Q38901 arabidopsis	
16	16	51	71.8	176	10	O9LYN4	O9LYN4 arabidopsis	
17	17	51	71.8	201	10	O22515	O22515 arabidopsis	
18	18	51	71.8	201	10	O80876	O80876 arabidopsis	
19	19	48	67.6	179	10	O40672	O40672 oryza sativ	

Result No.	SUMMARIES				Description
	Score	Query Match	Length	ID	
1	71	100.0	208	11	O8541 rattus norv
2	71	100.0	216	4	Q9BVK5 homo sapien
3	71	100.0	216	11	Q9DCY1
4	63	88.7	120	5	Q917V3 drosophila
5	63	88.7	204	5	O62190 caenorhabdi
6	63	88.7	205	5	Q9W227 drosophila
7	63	88.7	220	5	O44073 tachypleus
8	55	77.5	213	5	Q27774 schistosoma
9	54	76.1	87	6	Q29278 sus scrofa
10	52	73.2	204	10	Q9SF02 arabidopsis
11	52	73.2	213	5	Q26551 schistosoma
12	52	73.2	234	10	Q91Y53 arabidopsis
13	51	71.8	143	5	Q25093 hirudo medi
14	51	71.8	176	10	Q38867 arabidopsis
15	51	71.8	176	10	Q38901 arabidopsis
16	51	71.8	176	10	Q38901 arabidopsis
17	51	71.8	201	10	Q22515 arabidopsis
18	51	71.8	201	10	O80876 arabidopsis
19	48	67.6	179	10	Q40672 oryza sativ

```

RESULT 1
O88541
ID O88541 PRELIMINARY; PRT; 208 AA.
AC O88541;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYCLOPHILIN B (EC 5.2.1.8).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR-KYOTO; TISSUE=KIDNEY;
RA Kainer D.B., Doris P.A.;
RT "Cylophilin B.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases
CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
CC EMBL; AF071225; AAC25590.1; -.
DR HSSP; P23284; ILYN.
DR InterPro; IPR0021130; CSA_PPtase.
DR Pfam; PF00160; pro_isomerase, 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPtase_1; 1.
DR PROSITE; PS50072; CSA_PPtase_2; 1.
DR Isomerase; Rotamase.
KW
SQ SEQUENCE 208 AA; 22802 MW; 02408DFA7157218C CRC64;

Query Match 100.0%; Score 71; DB 11; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKHYPGW 11
DB 119 NFKLKHYPGW 129

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Query Match	100.0%	Score 71;	DB 11;	Length 208;
Best Local Similarity	100.0%	Pred. No. 0.00012;		
Matches 11; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	NFKLKHYPGCG	11	
Db	119	NFKLKHYPGCG	129	

```

RESULT 2
Q9BVK5 ID Q9BVK5 PRELIMINARY; PRT; 216 AA.
AC Q9BVK5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN, AND MELANOMA;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001125; AA01125.1; -.
KW Isomerase.
SQ SEQUENCE. 216 AA; 23742 MW; 2D0410A07AA9E420 CRC64;

Query Match 100.0%; Score 71; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. NO. 0.00012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKHGPGW 11
Db 127 NFKLKHGPGW 137

SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.Y.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov H.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fostel C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkuiov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Slapson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weissbrock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003458; AAG22196.1; -.
DR FlyBase; FBgn0034753; CG2852.

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DR InterPro: IPR002130; CSA_PP1ase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS50072; CSA_PP1ASE_2; 1.
SQ SEQUENCE 120 AA; 12962 MW; CF93898B694FA9F8 CRC64;

Query Match      88.7%; Score 63; DB 5; Length 120;
Best Local Similarity 90.9%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NFKLKHYPGW 11
   |||||
Db 27 NFKLKHYPGW 37

RESULT 5
CG2190
ID O62190 PRELIMINARY; PRT; 204 AA.
AC O62190;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYP-5 PROTEIN (EC 5.2.1.8).
GN CYP-5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Cottage A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Smaildon J., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Therry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; Z92784; CAB07192.1; -.
DR HSP; P23284; ICYN.
DR InterPro: IPR002130; CSA_PP1ase.
DR Pfam: PF00160; pro_isomerase; 1.
DR PRINTS: PR00153; CSAPPISMRASE.
DR PROSITE: PS00170; CSA_PP1ASE_1; 1.
DR PROSITE: PS50072; CSA_PP1ASE_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 204 AA; 21927 MW; 6216192BFE1FB493 CRC64;

Query Match      88.7%; Score 63; DB 5; Length 204;
Best Local Similarity 90.9%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NFKLKHYPGW 11
   |||||
Db 112 NFKLKHYPGW 122

us-09-720-469-5.rspt
Page 3

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SQ SEQUENCE 205 AA; 22199 MW; A9CEF88BLC813F7 CRC64;

Query Match 88.7%; Score 63; DB 5; Length 205;
Best Local Similarity 90.9%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NFKLKHGPGW 11
||||| ||

DB 112 NFKLKHGAGW 122

RESULT 7

ID O44073 PRELIMINARY; PRT; 220 AA.
AC O4073;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE G PRECURSOR (EC 5.2.1.8) (PPIASE)
DE (ROTAMASE) (CYCLOPHILIN G) (P27).
OS Tachyplesus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyplesus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=HEMOCYTE;
RX MEDLINE=98019238; PubMed=9353327;
RA Takaki Y., Muta T., Iwanaga S.;
RT "A peptidyl-prolyl cis/trans-isomerase (cyclophilin G) in regulated secretory granules.";
RL J. Biol. Chem. 272:28615-28621(1997).
CC -|- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. MAY PLAY A ROLE IN MAINTAINING THE CONFORMATIONAL INTEGRITY OF STORED GRANULAR PROTEINS.
CC -|- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -|- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).
CC -|- TISSUE SPECIFICITY: HEMOCYTE LARGE SECRETORY GRANULES.
CC -|- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
DR EMBL; AB002814; BAA23764.1; -.
DR HSSP; P23284; ICYN.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Signal; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 220 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE G.
SQ SEQUENCE 220 AA; 24198 MW; 728CB63EBB821C68 CRC64;

Query Match 88.7%; Score 63; DB 5; Length 220;
Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NFKLKHGPGW 11
||||| ||

DB 127 NFKLKHGAGW 137

RESULT 8

ID Q2774 PRELIMINARY; PRT; 213 AA.
AC Q2774;
DT 01-JAN-1999 (TREMBlrel. 09, Created)
DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE B) (ROTAMASE B) (CYCLOPHILIN B) (S-CYCLOPHILIN).
OS Schistosoma japonicum (Blood fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoida; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHINESE;
RX MEDLINE=97053959; PubMed=8898338;
RA Klinkert M.-Q., Bugli F., Cruz J., Engels B., Cioli D.;
RT "Sequence conservation of schistosome cyclophilins.";
RL Mol. Biochem. Parasitol. 81:239-242(1996).
CC -|- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -|- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -|- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).
CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
DR EMBL; U50389; AAC47316.1; -.
DR HSSP; P23284; ICYN.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
KW Multigene family.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 213 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
FT SITE 200 213 PREVENT SECRETION FROM ER (BY SIMILARITY).
FT FT
SQ SEQUENCE 213 AA; 23238 MW; D4986CDF7EDB8368 CRC64;

Query Match 77.5%; Score 55; DB 5; Length 213;
Best Local Similarity 81.8%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NFKLKHGPGW 11
||||| ||

DB 120 NFKLKHGAGW 130

RESULT 9

Q29278
ID Q29278 PRELIMINARY; PRT; 87 AA.
AC Q29278;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYCLOPHILIN B (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA library: analysis of 839 clones.";
RL Mamm. Genome 7:509-517(1996).
DR EMBL; F14628; CAA23162.1; -.
DR HSSP; P23284; ICYN.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS50072; CSA_PPIASE_2; 1.
DR NON_TER 1 1
FT NON_TER 87 87
SQ SEQUENCE 87 AA; 9551 MW; EB3EA68ED630AE97 CRC64;

Query Match 76.1%; Score 54; DB 6; Length 87;
 Best Local Similarity 100.0%; Pred. No. 0.043; 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LKHYGPGW 11
 Db 1 LKHYGPGW 8

RESULT 10
 Q9SP02 PRELIMINARY; PRT; 204 AA.
 ID Q9SP02;
 AC Q9SP02;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CYCLOPHILIN.
 GN ROC7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. WASSILEWSKIIJA;
 RA Jackson K.M., Soll D.;
 RT "Mutations in a new Arabidopsis cyclophilin disrupt interaction with
 protein phosphatase 2A".
 RL Mol. Gen. Genet. 0:0-0(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 features of the regions of 3,076,755 bp covered by sixty pl and TAC
 clones.";
 RL DNA Res. 7:31-63(2000).
 CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
 FOLDING OF PROTEINS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
 TRANS ISOMERASE FAMILY.
 DR EMBL; AF192490; AAF05760.1; -;
 DR EMBL; AB020755; BAA97339.1; -;
 DR HSSP; P23284; ICYN.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS50072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 204 AA; 21961 MW; CE2967AB4F65AF44 CRC64;

Query Match 73.2%; Score 52; DB 10; Length 204;
 Best Local Similarity 81.8%; Pred. No. 0.23; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NPKLKHGPGW 11
 Db 125 NPKLKHGPGF 135

RESULT 11
 Q26551 PRELIMINARY; PRT; 213 AA.
 ID Q26551
 AC Q26551;
 DT 01-JAN-1999 (Tremblrel. 09, Created)
 DT 01-JAN-1999 (Tremblrel. 09, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PRECURSOR (EC 5.2.1.8) (PPIASE)
 DE (ROTAMASE) (CYCLOPHILIN B) (S-CYCLOPHILIN).
 GN CYP.
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
 OC Trematoda; Digenea; Strigoida; Schistosomatoidea; Schistosomatidae;
 OC Schistosoma.
 OX NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PUERTO RICAN;
 RX MEDLINE=96362065; PubMed=8720179;
 RA Klinkert M.-Q., Hugli F., Engels B., Carrasquillo E., Valle C.,
 RA Cioli D.;
 RT "Characterization of a Schistosoma mansoni cDNA encoding a B-like
 cyclophilin and its expression in Escherichia coli.";
 RL Mol. Biochem. Parasitol. 75:99-111(1995).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
 CC -!- DEVELOPMENTAL STAGE: THIS SOLUBLE PROTEIN IS PRESENT IN ABUNDANCE
 IN THE ADULT WORM AS WELL AS IN THE SCHISTOSOMULA AND THE EGGS.
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
 DR EMBL; U30874; AAC46985.1; -;
 DR HSSP; P23284; ICYN.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS50072; CSA_PPIASE_2; 1.
 KW Cyclosporin; Isomerase; Rotamase; Signal; Endoplasmic reticulum;
 KW Multigene family.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 213 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.
 FT SITE 200 213 PREVENT SECRETION FROM ER (BY
 FT SIMILARITY).
 SQ SEQUENCE 213 AA; 23294 MW; 15FF6371B60B7415 CRC64;

Query Match 73.2%; Score 52; DB 5; Length 213;
 Best Local Similarity 72.7%; Pred. No. 0.24; 2; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NPKLKHGPGW 11
 Db 120 NPKLRHVAGW 130

RESULT 12
 Q9LY53 PRELIMINARY; PRT; 234 AA.
 ID Q9LY53
 AC Q9LY53;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CYCLOPHILIN-LIKE PROTEIN.
 GN F27K19.100.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Benes V., Wurmbach E., Drzonek H., Ansoorge W., Mewes H.W., Rudd S.,
 RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; AL163832; CAB87846.1; -.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 2.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 234 AA; 25105 MW; 5CB22BBB363C2450 CRC64;

Query Match 73.2%; Score 52; DB 10; Length 234;
Best Local Similarity 81.8%; Pred. No. 0.27;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPGW 11
||||| |||
DB 155 NFKLKHGPGF 165

RESULT 13
Q25093 ID Q25093 PRELIMINARY; PRT; 143 AA.
AC Q25093;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYCLOPHILIN-A (EC 5.2.1.8).
GN HCP.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96165729; PubMed=8587897;
RA Korneev S., Blackshaw S.E., Kaiser K., Davies J.A.;
RT "CDNA libraries from identified neurons";
RL Proc. R. Soc. Lond., B, Biol. Sci. 263:57-62(1996).
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; U36797; AAB01531.1; -.
DR HSSP; P05092; 2CPL.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 143 AA; 15398 MW; 64FFD82018480A6B CRC64;

Query Match 71.8%; Score 51; DB 5; Length 143;
Best Local Similarity 90.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
||||| |||
DB 66 NFKLKHGPG 75

RESULT 14
Q38867

ID Q38867 PRELIMINARY; PRT; 176 AA.
AC Q38867;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYCLOPHILIN (EC 5.2.1.8).
GN CYP4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LANDSBERG;
RA Saito T., Ashida H., Kawamukai M., Matsuda H., Nakagawa T.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; U31370; AAA74096.1; -.
DR HSSP; P05092; 1CWL.
DR Mendel; 6281; Arath;1040:6281.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; 1.
DR PROSITE; PS00072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 176 AA; 18969 MW; 24C2031B6CA107A0 CRC64;

Query Match 71.8%; Score 51; DB 10; Length 176;
Best Local Similarity 90.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGPG 10
||||| |||
DB 94 NFKLKHGPG 103

RESULT 15
Q38901 ID Q38901 PRELIMINARY; PRT; 176 AA.
AC Q38901;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOSOLIC CYCLOPHILIN (EC 5.2.1.8).
GN ROC2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98088013; PubMed=9426607;
RA Chou I.T., Gasser C.S.;
RT "Characterization of the cyclophilin gene family of Arabidopsis
thaliana and phylogenetic analysis of known cyclophilin proteins.";
RL Plant Mol. Biol. 35:873-892(1997).
CC -!- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASES ACCELERATE THE
CC FOLDING OF PROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-
CC TRANS ISOMERASE FAMILY.
DR EMBL; U40400; AAB96833.1; -.

DR HSP: P05092; 1CWL.
 DR Mendel; 6283; Arath; 1040; 6283.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; pro_isomerase; 1.
 DR PRINTS; PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS0072; CSA_PPIASE_2; 1.
 KW Isomerase; Rotamase.
 SQ SEQUENCE 175 AA; 18906 MW; 24C2031B6BC4DD90 CRC64;

Query Match 71.8%; Score 51; DB 10; Length 176;
 Best Local Similarity 90.0%; Pred. No. 0.3;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 NFKLKHGPG 10
 Db 94 NFKLAHTGPG 103
 |||||

Search completed: January 15, 2002, 13:16:26
 Job time: 657 sec

